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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 13.8519 Seconds
(without alignments)
152,738 Million cell updates/sec

Title: US-09-847-637B-1

Sequence: 1 GPKGRNVVLEKMGAPITINDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR:76: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	122	100.0	540 2	A26950 groEL2 protein - M
2	122	100.0	540 2	A43509 65k antigen mbah -
3	122	100.0	540 2	C41325 heat shock protein
4	122	100.0	541 2	S40245 heat shock protein
5	122	100.0	541 2	T44725 chaperonin 60k (im
6	122	100.0	588 2	A25902 65k antigen - Myco
7	112	91.8	538 2	H72367 groEL protein - Th
8	107	87.7	540 2	B41325 heat shock protein
9	107	87.7	541 2	T35591 chaperonin cpn60 -
10	103	84.4	538 2	Q01195 heat shock protein
11	103	84.4	539 2	B49855 heat shock protein
12	103	84.4	541 2	S72614 chaperonin 60 - Th
13	103	84.4	542 2	AC1704 class I heat-shock
14	103	84.4	542 2	AD1333 class I heat-shock
15	103	84.4	543 2	B41872 heat shock protein
16	103	84.4	543 2	F97232 chaperonin GroEL,
17	103	84.4	544 2	B41884 heat shock protein
18	103	84.4	544 2	JC6063 58k heat shock pro
19	103	84.4	544 2	JC6063 chaperonin groEL -
20	103	84.4	544 2	B83720 class I heat-shock
21	102	83.6	543 2	S70013 chaperonin-like pr
22	101	82.8	528 2	S73270 chaperonin, 60k -
23	101	82.8	541 2	T06829 chaperonin groEL -
24	101	82.8	541 2	AG2263 chaperonin GroEL
25	101	82.8	546 2	S34938 heat shock protein
26	100	82.0	544 1	B68249 chaperonin groEL h
27	100	82.0	544 1	BYRGL chaperonin groEL -
28	100	82.0	546 2	B47073 chaperonin GroEL -
29	99	81.1	539 2	S22342 chaperonin HSP60 -

30	99	81.1	542 2	JN0661 heat shock protein
31	99	81.1	542 2	S32106 groEL protein - La
32	99	81.1	540 2	B86674 60 KD chaperonin
33	98	80.3	540 2	G95222 chaperonin, 60 kDa
34	98	80.3	540 2	H88086 chaperonin GroEL
35	98	80.3	544 2	B82048 chaperonin, 60 kD
36	98	80.3	547 2	JC4519 heat-shock protein
37	98	80.3	547 2	B43606 heat shock protein
38	98	80.3	547 2	B83098 GroEL protein PA43
39	98	80.3	548 1	BYRGL chaperonin groEL -
40	98	80.3	548 2	D91269 chaperonin GroEL
41	98	80.3	548 2	G75439 groEL protein - De
42	98	80.3	548 2	B86110 hypothetical prote
43	98	80.3	548 2	AS1045 GroEL protein (imp
44	98	80.3	550 2	A41468 60k heat shock pro
45	98	80.3	552 2	S39765 chaperonin 60 - Co

ALIGNMENTS

```

RESULT 1
A26950 groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
N/Alternate names: 65k antigen
C/Species: Mycobacterium tuberculosis
C/Date: 02-Jun-1998 #sequence_revision 02-Jun-1998 #text_change 20-Jun-2000
C/Accession: A26950; A70830
R/Shimnick, T.M.
J. Bacteriol. 169, 1080-1088, 1987
A/Title: The 65-Kilodalton antigen of Mycobacterium tuberculosis.
A/Reference number: A26950; MUID:87137260; PMID:3029018
A/Accession: A26950
A/Molecule type: DNA
A/Residues: 1-540 <SH1>
A/Cross-references: GB:M5467; NID:g149999; PIDN:AAA88232.1; PID:g150000
R/Cole, S.T.; Brosch, K.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulterson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: A70830
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Residues: 1-540 <COL>
A/Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CAA17397.1; PID:g29095;
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: groEL2; Rv0440
C/Superfamily: chaperonin groEL

Query Match 100.0% Score 122, DB 2, Length 540,
Best local similarity 100.0%; Pred. No. 9, le-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GPKGRNVVLEKMGAPITINDG 22
Db 31 GPKGRNVVLEKMGAPITINDG 52

RESULT 2
A43509 65k antigen mbah - Mycobacterium bovis
C/Species: Mycobacterium bovis
C/Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C/Accession: A43509
R/Thole, J.E.R.; Keulen, W.J.; Kolj, A.H.J.; Groothuis, D.G.; Berwald, L.G.; Tiesjema, f
Infact. Immun. 55, 1466-1475, 1987
A/Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton
A/Reference number: A43509; MUID:8719115; PMID:3553003
A/Accession: A43509

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A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <THO>
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPITNDG 22
DB 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 3
C41325
heat shock protein 56 - Streptomyces albus
N/Alternate names: heat shock protein groEL homolog 2
C/Species: Streptomyces albus
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 26-Aug-1999
C/Accession: C41325
R/Mazodier, P.; Gujiljemi, G.; Davies, J.; Thompson, C.J.
J. Bacteriol. 173, 7382-7386, 1991
A/Title: Characterization of the groEL-like genes in Streptomyces albus.
A/Reference number: A41325; MUID:92041639; PMID:1682304
A/Accession: C41325
A:Molecule type: DNA
A:Residues: 1-540 <MAZ>
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294
C/Genetics:
A:Gene: groEL2
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPITNDG 22
DB 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 4
S40245
heat shock protein 65 - Mycobacterium paratuberculosis
C/Species: Mycobacterium paratuberculosis
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C/Accession: S40245
R/Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdoso, R.
submitted to the EMBL Data Library, August 1993
A/Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.
A/Reference number: S40245
A/Accession: S40245
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-541 <COL>
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPITNDG 22
DB 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 5
T44725
chaperonin 60K [imported] - Mycobacterium leprae
N/Alternate names: heat shock protein GroEL-2

C/Species: Mycobacterium leprae
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C/Accession: T44725
R/James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A/Reference number: Z22831
A/Accession: T44725

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-541 <JAM>
A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1
A/Experimental source: cosmid B1450
C/Genetics:
A:Gene: groEL-2
C:Superfamily: chaperonin groEL
C/Keywords: molecular chaperone

Query Match 100.0%; Score 122; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPITNDG 22
DB 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 6
A25902
65K antigen - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 12-Sep-1997
C/Accession: A25902
R/Mehra, V.; Sweetser, D.; Young, R.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986
A/Title: Efficient mapping of protein antigenic determinants.
A/Reference number: A25902; MUID:86313701; PMID:2428046
A/Accession: A25902
A:Molecule type: DNA
A:Residues: 1-588 <MEH>
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 9, 9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPITNDG 22
DB 78 GPKGRNVLEKKWGAPITNDG 99

RESULT 7
H72367
groEL protein - Thermotoga maritima (strain MSB8)

C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: H72367
R/Nelson, K.R.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.

Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: H72367
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <ARN>
A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:AAD35591.1; PID:g49810
A/Experimental source: strain MSB8
C/Genetics:
A:Gene: TM0506
C:Superfamily: chaperonin groEL

Query Match 91.8%; Score 112; DB 2; Length 538;

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:08 ; Search time 9.37037 Seconds
(without alignments)
110.411 Million cell updates/sec

Title: US-09-847-637B-1
Perfect score: 122
Sequence: 1 GPKGRNVVLEKKMGAPITNDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	476	1 CH62_STRLI	033658 streptomyc
2	122	100.0	539	1 CH60_TSTUY	P97086 tsukamurell
3	122	100.0	539	1 CH62_MYCTU	P06806 mycobacteri
4	122	100.0	539	1 CH62_STRLA	Q00768 streptomyc
5	122	100.0	540	1 CH60_MYCPA	P42384 mycobacteri
6	122	100.0	540	1 CH60_TSTUPA	Q9af5 tsukamurell
7	122	100.0	540	1 CH62_MYCTE	P99229 mycobacteri
8	122	100.0	541	1 CH60_COREQ	Q93q12 corynebacte
9	122	100.0	541	1 CH60_NOCPA	Q9af5 nocardia fa
10	122	100.0	541	1 CH62_STRCO	Q9af5 streptomyc
11	122	100.0	542	1 CH60_NOCAS	Q9af5 nocardia as
12	117	95.9	544	1 CH60_PROAC	Q8cy24 propionibac
13	116	95.1	547	1 CH62_COREF	Q8cy22 corynebacte
14	116	95.1	548	1 CH62_COREG	Q8m54 corynebacte
15	114	93.4	540	1 CH60_TROWT	Q9k160 corynebacte
16	112	91.8	538	1 CH60_THEMA	Q9wyx6 thermotoga
17	112	91.8	538	1 CH60_THEMA	Q9wyx6 thermotoga
18	107	87.7	539	1 CH61_STRLA	Q00717 streptomyc
19	107	87.7	540	1 CH61_STRCO	P40111 streptomyc
20	105	86.1	537	1 CH60_PARDN	Q9k111 parascardov
21	105	86.1	541	1 CH60_GARVA	Q9k157 gardnerella
22	104	85.2	541	1 CH60_BIFPA	Q9m78 bifidobacte
23	104	85.2	541	1 CH60_BIFPA	Q9m78 bifidobacte
24	104	85.2	542	1 CH60_BIFPA	Q9m78 bifidobacte
25	103	84.4	538	1 CH60_BACPA	P26209 bacillus ps
26	103	84.4	539	1 CH60_BACPA	P26209 bacillus ps
27	103	84.4	539	1 CH60_BACPA	P26209 bacillus ps
28	103	84.4	540	1 CH60_THBR	Q60024 thermoaer
29	103	84.4	542	1 CH60_LISIN	Q929V0 listeria in
30	103	84.4	542	1 CH60_LISIN	Q929V0 listeria in
31	103	84.4	543	1 CH60_BACSU	P28358 bacillus su
32	103	84.4	543	1 CH60_BACSU	P28358 bacillus su
33	103	84.4	543	1 CH60_BACSU	P28358 bacillus su

34	103	84.4	544	1 CH60_BACPD	O50305 bacillus ha
35	102	83.6	540	1 CH60_RHOKR	O9xcas rhodothermu
36	102	83.6	540	1 CH60_THERN	O9x5t7 thermoaer
37	102	83.6	543	1 CH60_ANASL	Q9amj8 anabaena sp
38	102	83.6	543	1 CH60_LACJO	Q9k123 lactobacill
39	102	83.6	543	1 CH62_SYNEL	O57002 synechococc
40	101	82.8	528	1 CH60_PORPU	P51349 porphyra pu
41	101	82.8	538	1 CH60_SCAIO	Q9ey76 scardovia i
42	101	82.8	541	1 CH60_CVAPA	Q37757 cyanophora
43	101	82.8	544	1 CH61_ANASP	O9y9z8 anabaena sp
44	101	82.8	544	1 CH61_SYNVU	O50323 synechococc
45	101	82.8	545	1 CH60_SYNEL	Q8mdm4 synechococc

ALIGNMENTS

RESULT 1
CH62_STRLI STANDARD; PRT; 476 AA.
ID CH62_STRLI
AC 033658;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE 60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).
GN GROEL2 OR GROEL2.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces.
OX NCBI_TaxID:1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TX21;
RX MEDLINE=98048481; PubMed=9387235;
RA de Leon P., Marco S., Isiegas C., Marina A., Carrascosa J.L.,
RA Meliado R.P.;
RT "Streptomyces lividans groEL1 and groEL2 genes";
RL Microbiology 143:3563-3571 (1997).
CC -1- FUNCTION: Prevents misfolding and promotes the refolding and
CC proper assembly of unfolded polypeptides generated under stress
CC conditions (By similarity).
CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
CC 7 subunits (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X95971; CA65226.1; -.
DR HSMAP; P06139; IGRU.
DR HSMAP; MF 00600; atypical; 1.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1; 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPI.
DR PROSITE; PS00296; CHAPERONIN60; 1.
KW Chaperone; ATP-binding; Multigene family.
FT INIT MET 0 0
SQ SEQUENCE 476 AA; 50529 MW; 760F81793F4FED4D CRC64;
Query Match 100.0%; Score 122; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 8.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVVLEKKMGAPITNDG 22
|||||

DB 30 GPKGRNVLEKKMGAPTTNDG 51

RESULT 2

CH60 TSUTY STANDARD; PRT; 539 AA.

ID CH60 TSUTY STANDARD; PRT; 539 AA.

AC P97086; 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (heat shock protein 60).

DE GROEL OR GROEL OR HSP60.

OS Tsukamurella tyrosinosa.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Tsukamurellaceae; Tsukamurella.

NCBI_TaxID=57704;

OX NCBI_TaxID=57704;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IMTB D-1411;

RA Zimmermann O., Pinkenburg O., Koechel H.G.;

RT "Tsukamurella tyrosinosa sp. nov. hsp60 gene for heat shock protein 60."

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.

CC -----

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CC -----

CC EMBL; U90204; AAB49990.1; -.

DR HSP; P06139; 1GRL.

DR HAMAP; MF 00600; -; 1.

DR InterPro; IPR001844; Chaperin Cpn60.

DR InterPro; IPR002423; Cpn60/TCF-1.

DR Pfam; PF00118; Cpn60_TCF1.1.

DR PRINTS; PR00298; CHAPERONIN60.

DR PRINTS; PR00304; TCOMPLEXTCF1.

DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.

KW Chaperone; ATP-binding.

SO SEQUENCE 539 AA; 5637 MW; 635314830CB662 CRC64;

Query Match 100.0%; Score 122; DB 1; Length 539;

Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAPTTNDG 22

DB 31 GPKGRNVLEKKMGAPTTNDG 52

RESULT 3

CH62 MYCTU STANDARD; PRT; 539 AA.

ID CH62 MYCTU STANDARD; PRT; 539 AA.

AC P06806; Q48920; Q48931;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin 2 (Protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (Heat shock protein 65) (Cell wall protein A) (Antigen A).

DE GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.

OS Mycobacterium tuberculosis, and

OS Mycobacterium bovis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

NCBI_TaxID=1773, 1765;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=Brdman;

RX MEDLINE=87137260; PubMed=3029018;

RA Shimnick T.M.;

RT "The 65-kilodalton antigen of Mycobacterium tuberculosis.";

RL J. Bacteriol. 169:1080-1088(1987).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.B. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;

RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

RL Nature 393:537-544(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;

RA Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Debey R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Knouri H., Gill J., Mikula A., Bishel W.;

RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=M.bovis; STRAIN=BCG;

RX MEDLINE=8713155; PubMed=3551003;

RA Thole J.B.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Bernald L.G., Tiesjema R.H., van Embden J.D.A.;

RT "Characterization, sequence determination, and immunogenicity of a 64-kilodalton protein of Mycobacterium bovis BCG expressed in Escherichia coli K-12.";

RL Infect. Immun. 55:1466-1475(1987).

RN [5]

RP SEQUENCE OF 45-195 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, and 12-14001;

RA Ros C., Belak K.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE OF 63-182 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMC 410, and TMC 1024;

RX MEDLINE=95150784; PubMed=7848059;

RA Kapur V., Li L.L., Hamrick M.R., Plikaytis B.B., Shimnick T.M., Teleni A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y., Clarridge J.B., Kreiswirth B.N., Musser J.M.;

RT "Rapid Mycobacterium species assignment and unambiguous identification of mutations associated with antimicrobial resistance in Mycobacterium tuberculosis by automated DNA sequencing.";

RL Arch. Pathol. Lab. Med. 119:131-138(1995).

RN [7]

RP SEQUENCE OF 64-177 FROM N.A.

RC SPECIES=M.tuberculosis;

RX MEDLINE=95214306; PubMed=7699930;

RA Hidaka E., Ueno I., Kawakami Y., Furutawari C., Furinata K., Katsuyama T.;

RT "Detection and identification of mycobacteria by PCR-RFLP method.";

RL Rinsho Byori 43:155-161(1995).

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 35.4444 Seconds
(without alignments)
160.171 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVVLEKMGAPITINDG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioplasmid:*
- 17: sp_archaeoplasmid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	122	100.0	59	2	Q9EMD1
2	122	100.0	61	2	Q9EUB7
3	122	100.0	539	2	P97086
4	122	100.0	540	2	Q9AFN5
5	122	100.0	541	2	Q93Q12
6	122	100.0	541	2	Q9AFN6
7	122	100.0	541	2	Q9AGW1
8	122	100.0	542	2	Q9APC5
9	122	100.0	548	2	Q9GAR7
10	122	100.0	548	2	Q9GAR7
11	122	100.0	548	2	Q9G923
12	122	100.0	548	2	Q9G8X0
13	122	100.0	549	2	Q9GAR9
14	122	100.0	533	2	Q9FDS2
15	116	95.1	547	16	Q8CT22
16	116	95.1	548	16	Q8NM64

17	105	86.1	537	2	Q9KI71	Q9KI71 parascardov
18	105	86.1	541	2	Q9KI57	Q9KI57 gaderella
19	104	85.2	537	2	Q9IM78	Q9IM78 bifidobacte
20	104	85.2	541	16	Q9G879	Q9G879 bifidobacte
21	104	85.2	582	2	Q9REU4	Q9REU4 bifidobacte
22	103	84.4	539	2	Q9REU4	Q9REU4 bifidobacte
23	103	84.4	539	2	Q9RC20	Q9RC20 bacillus st
24	103	84.4	543	2	Q9GB95	Q9GB95 bacillus st
25	102	83.6	543	2	Q9AMJ8	Q9AMJ8 anabaena sp
26	101	82.8	538	2	Q9EY76	Q9EY76 scardovia i
27	101	82.8	545	16	Q9DMD4	Q9DMD4 synechococc
28	101	82.8	546	2	Q91198	Q91198 leptospira
29	100	82.0	543	2	Q9KXN2	Q9KXN2 thermus sp.
30	100	82.0	545	16	Q9CXJ3	Q9CXJ3 oceanobacill
31	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
32	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
33	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
34	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
35	99	81.1	531	2	Q9GBD0	Q9GBD0 enterococcu
36	99	81.1	532	2	Q9GBD0	Q9GBD0 enterococcu
37	99	81.1	532	2	Q9GBD0	Q9GBD0 enterococcu
38	99	81.1	532	2	Q9GBD0	Q9GBD0 enterococcu
39	98	80.3	82	2	Q9F4E5	Q9F4E5 fusobacteri
40	98	80.3	191	2	Q9VUS2	Q9VUS2 secondary s
41	98	80.3	329	2	Q9EWA9	Q9EWA9 serratia ma
42	98	80.3	329	2	Q9EWA8	Q9EWA8 serratia ma
43	98	80.3	329	2	Q9EXM7	Q9EXM7 enterobacte
44	98	80.3	329	2	Q9EXM5	Q9EXM5 enterobacte
45	98	80.3	329	2	Q9F2H2	Q9F2H2 serratia ma

ALIGNMENTS

RESULT 1

Q9EMD1 PRELIMINARY; PRT; 59 AA.

AD Q9EMD1; ID Q9EMD1; AC Q9EMD1; DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Heat-shock protein (Fragment).

GN GROEL2.

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

CC Streptomycetaceae; Streptomycetaceae; Streptomycetes.

OX NCBI_TaxID=1902;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=J802;

RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;

RT "A cold-shock-like gene with pleiotropic effects on streptomycetes

RT antibiotic/biosynthesis." ;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ250536; CAC19351.1; -.

DR HSSP; P06139; IAO.

DR InterPro; IPR002423; Cpn60/TCF-1.

DR Pfam; PF00118; cpn60_TCF1.1.

DR PRINTS; PR00304; TCOMPLXTCPL.

KW ATP-binding; Chaperone.

FT NON TER 59

FT SEQUENCE 59 AA; 6407 MW; E7B2419B7DB68FA CRC64;

Query Match 100.0%; Score 122; DB 2; Length 59;

Best Local Similarity 100.0%; Pred. No. 9.8e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVVLEKMGAPITINDG 22

Db 31 GPKGRNVVLEKMGAPITINDG 52

RESULT 2

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Q9EUR7      PRELIMINARY;      PRT;      61 AA.
ID Q9EUR7
AC Q9EUR7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Heat-shock protein (Fragment).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF 141;
RA Martinez-Costra O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RT antibiotic biosynthesis.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250537; CAC19355.1; -.
DR HSSP; P06139; 1AON.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; cpn60 TCP1.1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
KM ATP-binding; Chaperone.
FT NON TER
SQ SEQUENCE 61 AA; 6645 MW; D20095F4199B7CA CRC64;

Query Match      100.0%; Score 122; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVLEKKGAPITINDG 22
DB      31 GPKGRNVLEKKGAPITINDG 52

RESULT 3
P97086      PRELIMINARY;      PRT;      539 AA.
ID P97086
AC P97086;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella tyrosinosevens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMIB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosevens sp. nov. hsp60 gene for heat shock
RT protein 60.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U90204; AAB49990.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; cpn60 TCP1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KM ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49B7FC CRC64;

Query Match      100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVLEKKGAPITINDG 22
DB      31 GPKGRNVLEKKGAPITINDG 52

RESULT 4
P9AFAS      PRELIMINARY;      PRT;      540 AA.
ID P9AFAS
AC Q9AFAS;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP352578; AAK18614.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; cpn60 TCP1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KM ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49B7FC CRC64;

Query Match      100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVLEKKGAPITINDG 22
DB      31 GPKGRNVLEKKGAPITINDG 52

RESULT 5
P93012      PRELIMINARY;      PRT;      541 AA.
ID P93012
AC Q93012;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match      100.0%; Score 122; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVLEKKGAPITINDG 22
DB      31 GPKGRNVLEKKGAPITINDG 52

RESULT 4
P9AFAS      PRELIMINARY;      PRT;      540 AA.
ID P9AFAS
AC Q9AFAS;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
DE protein).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP352578; AAK18614.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCP-1.
DR Pfam; PF00118; cpn60 TCP1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KM ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 56506 MW; 524B5CDB2C49B7FC CRC64;

Query Match      100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVLEKKGAPITINDG 22
DB      31 GPKGRNVLEKKGAPITINDG 52

RESULT 5
P93012      PRELIMINARY;      PRT;      541 AA.
ID P93012
AC Q93012;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

```

[illegible]

PT especially arthritis .

XX Claim 1; Page 7; 58pp; English.
 XX
 XX The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX

SO Sequence 22 AA;

Query Match 100.0%; Score 122; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.9e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPITNDG 22
 DB 1 GPKGRNVLEKKWGAPITNDG 22

RESULT 2

AA60145
 ID AA60145 standard; protein; 215 AA.

XX AA60145;

DT 25-AUG-1998 (first entry)

DE M. vaccae antigen GV-27A sequence.

XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
 KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
 KM mycobacteria infection; vaccine; cancer.

XX Mycobacterium vaccae.

PN W09808542-A2.

XX 05-MAR-1998.

PF 28-AUG-1997; 97WO-NZ00105.

PR 12-JUN-1997; 97US-0873970.

PR 29-AUG-1996; 96US-0705347.

PA (GENE-) GENESIS RES & DEV CORP.

PI HiYama J, Prestidge RL, Scott LM, Skinner MA, Tan P;

PI Visser E;

DR WPI; 1998-216926/19.

DR N-PSDB; AAV34609.

XX Mycobacterium vaccae polypeptides - used to develop products for use
 PT in detection, therapy and prevention of mycobacteria infections or
 PT as immune response enhancers

XX Claim 48; Pages 117-118; 153pp; English.

XX This represents a Mycobacterium vaccae antigen GV-27A. The invention
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an
 CC immune response in patients previously exposed to a mycobacterium. Such
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific
 CC immune response. The methods and products can be used for the detection,
 CC treatment and prevention of infectious diseases caused by mycobacteria
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
 CC the ability to induce cell proliferation and cytokine production (e.g.
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,
 CC B cells, or macrophages. They can be used for enhancing immune responses
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.

SO Sequence 215 AA;

Query Match 100.0%; Score 122; DB 19; Length 215;
 Best Local Similarity 100.0%; Pred. No. 5.9e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPITNDG 22
 DB 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 3

AAV14892
 ID AAV14892 standard; protein; 215 AA.

XX AAV14892;

DT 25-OCT-1999 (first entry)

DE Amino acid sequence of M. vaccae antigen GV-27A.

XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KM dendritic cell maturation; infectious disease; immune disorder; cancer;
 KM respiratory system; mycobacterial infection; allergy; tuberculosis;
 KM leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KM dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 KM squamous cell carcinoma; melanoma.

XX Mycobacterium vaccae.

PN W09932634-A2.

PD 01-JUL-1999.

PF 23-DEC-1998; 98WO-NZ00189.

PR 04-DEC-1998; 98US-0205426.

PR 23-DEC-1997; 97US-0996624.

PR 23-DEC-1997; 97US-0997080.

PR 23-DEC-1997; 97US-0997362.

PR 11-JUN-1998; 98US-0095855.

PR 17-SEP-1998; 98US-0156181.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;

DR WPI; 1999-430163/36.

DR N-PSDB; AAZ11344.

XX Enhancing immune response to an antigen

XX Example 14; Page 191-192; 243pp; English.

XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate
 CC T cells and natural killer cells, to stimulate the production of
 CC cytokines; to enhance the expression of co-stimulatory molecules on
 CC dendritic cells and monocytes; and to enhance dendritic cell maturation
 CC and function. The proteins can be expressed by standard recombinant
 CC methodology. Pharmaceutical compositions comprising the proteins or
 CC nucleic acid sequences encoding the proteins can be used for the
 CC treatment, prevention, and detection of disorders including infectious
 CC diseases, immune disorders and cancer. In particular, the compounds and
 CC methods are used for treatment of diseases of the respiratory system,
 CC such as mycobacterial infections, asthma, allergies, tuberculosis,
 CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma.

XX Sequence 215 AA;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:09:39 ; Search time 30.1481 Seconds
(without alignments)
145.229 Million cell updates/sec

Title: US-09-847-637B-1
Sequence: 1 GPKGRNVVLEKKMGAPITINDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	122	100.0	22	US-09-847-637B-1
2	122	100.0	215	US-09-880-505-117
3	122	100.0	215	US-10-205-979-41
4	122	100.0	215	US-10-051-643-117
5	122	100.0	295	US-10-267-311-33
6	122	100.0	523	US-09-880-505-114
7	122	100.0	523	US-10-051-643-114
8	122	100.0	540	US-09-847-637B-6
9	122	100.0	540	US-09-712-363-169
10	122	100.0	540	US-10-267-311-4
11	122	100.0	540	US-10-046-649-3
12	122	100.0	540	US-10-046-649-4
13	122	100.0	541	US-09-880-505-160
14	122	100.0	541	US-10-205-979-40
15	122	100.0	541	US-10-051-643-160

16	122	100.0	541	US-10-156-761-11465	Sequence 11465, A
17	122	100.0	576	US-10-369-493-8322	Sequence 8322, Ap
18	122	100.0	639	US-10-267-311-17	Sequence 17, Appl
19	122	100.0	648	US-10-267-311-29	Sequence 29, Appl
20	122	100.0	690	US-10-068-059-10	Sequence 10, Appl
21	122	100.0	709	US-10-068-059-8	Sequence 8, Appl
22	122	100.0	724	US-10-068-059-12	Sequence 12, Appl
23	122	100.0	746	US-10-068-059-6	Sequence 6, Appl
24	122	100.0	948	US-10-267-311-21	Sequence 21, Appl
25	116	95.1	548	US-09-738-626-6486	Sequence 6486, Ap
26	112	91.8	538	US-10-369-493-2950	Sequence 2950, Ap
27	107	87.7	542	US-10-156-761-12526	Sequence 12526, A
28	103	84.4	544	US-10-369-493-17132	Sequence 17132, A
29	103	84.4	544	US-10-369-493-23094	Sequence 23094, A
30	101	82.8	521	US-10-369-493-9597	Sequence 9597, Ap
31	101	82.8	540	US-10-369-493-15838	Sequence 15838, A
32	101	82.8	544	US-10-369-493-15468	Sequence 15468, A
33	101	82.8	544	US-10-369-493-16217	Sequence 16217, A
34	101	82.8	544	US-10-369-493-20276	Sequence 20276, A
35	100	82.0	544	US-10-369-493-20873	Sequence 20873, A
36	100	82.0	545	US-10-369-493-19756	Sequence 19756, A
37	99	81.1	547	US-10-369-493-10014	Sequence 10014, A
38	98	80.3	547	US-10-046-649-2	Sequence 2, Appl
39	98	80.3	548	US-09-415-849-1	Sequence 1, Appl
40	98	80.3	548	US-09-276-455-10	Sequence 10, Appl
41	98	80.3	548	US-10-369-493-513	Sequence 513, Appl
42	98	80.3	551	US-10-369-493-20184	Sequence 20184, A
43	98	80.3	641	US-10-267-311-51	Sequence 51, Appl
44	97	79.5	545	US-10-228-167A-2	Sequence 2, Appl
45	95	77.9	551	US-10-369-493-18994	Sequence 18994, A

ALIGNMENTS

RESULT 1
US-09-847-637B-1
; Sequence 1, Application US/09847637B
; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Umanetsky, Rina
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-1
Query Match 100.0%; Score 122; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVVLEKKMGAPITINDG 22
DB 1 GPKGRNVVLEKKMGAPITINDG 22
RESULT 2
US-09-880-505-117
; Sequence 117, Application US/09880505

```
Publication No. US20030007976A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Rose
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c2
CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 08/997,080
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 117
LENGTH: 215
TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-09-880-505-117

Query Match      100.0%; Score 122; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 4,1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEKKWGAPTTNDG 22
DB 31 GPKGRNVVLEKKWGAPTTNDG 52

RESULT 3
US-10-205-979-41
Sequence 41, Application US/10205979
Publication No. US20030147861A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Abernethy, Nevyn
TITLE OF INVENTION: Compounds and Methods for the Modulation
of Immune Responses
FILE REFERENCE: 11000.1063U
CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 215
TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-10-205-979-41

Query Match      100.0%; Score 122; DB 12; Length 215;
Best Local Similarity 100.0%; Pred. No. 4,1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEKKWGAPTTNDG 22
DB 31 GPKGRNVVLEKKWGAPTTNDG 52

RESULT 4
US-10-051-643-117
Sequence 117, Application US/10051643
Publication No. US20020197265A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Diseases of the Respiratory
System using Mycobacterium vaccae
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FILE REFERENCE: 11000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 117
LENGTH: 215
TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-10-051-643-117

Query Match      100.0%; Score 122; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 4,1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEKKWGAPTTNDG 22
DB 31 GPKGRNVVLEKKWGAPTTNDG 52

RESULT 5
US-10-267-311-33
Sequence 33, Application US/10267311
Publication No. US20030050469A1
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 295
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-33

Query Match      100.0%; Score 122; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 5,7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEKKWGAPTTNDG 22
DB 31 GPKGRNVVLEKKWGAPTTNDG 52

RESULT 6
US-09-880-505-114
Sequence 114, Application US/09880505
Publication No. US20030007976A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Rose
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c2
CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 15.4815 Seconds

(without alignments)
60.126 Million cell updates/sec

Title: US-09-847-637B-1

Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	215	2 US-08-997-080-117	Sequence 117, App
2	122	100.0	215	3 US-08-997-362-117	Sequence 117, App
3	122	100.0	215	3 US-09-095-855-117	Sequence 117, App
4	122	100.0	215	4 US-09-324-542-117	Sequence 117, App
5	122	100.0	215	4 US-09-205-426-117	Sequence 117, App
6	122	100.0	295	4 US-09-613-303-33	Sequence 33, Appl
7	122	100.0	523	2 US-08-997-080-114	Sequence 114, App
8	122	100.0	523	2 US-08-997-362-114	Sequence 114, App
9	122	100.0	523	3 US-09-095-855-114	Sequence 114, App
10	122	100.0	523	4 US-09-324-542-114	Sequence 114, App
11	122	100.0	523	4 US-09-205-426-114	Sequence 114, App
12	122	100.0	540	2 US-08-368-834-20	Sequence 20, Appl
13	122	100.0	540	4 US-08-461-722-3	Sequence 3, Appl
14	122	100.0	540	4 US-08-461-722-4	Sequence 4, Appl
15	122	100.0	540	4 US-08-336-251-3	Sequence 3, Appl
16	122	100.0	540	4 US-08-336-251-4	Sequence 4, Appl
17	122	100.0	540	4 US-09-468-041-3	Sequence 3, Appl
18	122	100.0	540	4 US-09-468-041-4	Sequence 4, Appl
19	122	100.0	540	4 US-09-613-303-4	Sequence 4, Appl
20	122	100.0	540	5 PCT-US94-06362-3	Sequence 3, Appl
21	122	100.0	540	5 PCT-US94-06362-4	Sequence 4, Appl
22	122	100.0	541	2 US-08-447-154-19	Sequence 19, Appl
23	122	100.0	541	2 US-08-447-154-34	Sequence 34, Appl
24	122	100.0	541	2 US-08-997-080-160	Sequence 160, App
25	122	100.0	541	2 US-08-997-362-160	Sequence 160, App
26	122	100.0	541	3 US-09-095-855-160	Sequence 160, App
27	122	100.0	541	3 US-08-432-697-34	Sequence 34, Appl

28	122	100.0	541	3 US-08-466-248-34	Sequence 34, Appl
29	122	100.0	541	4 US-09-324-542-160	Sequence 160, App
30	122	100.0	541	4 US-09-205-426-160	Sequence 160, App
31	122	100.0	639	4 US-09-613-303-17	Sequence 17, Appl
32	122	100.0	648	4 US-09-613-303-29	Sequence 29, Appl
33	122	100.0	948	4 US-09-613-303-21	Sequence 21, Appl
34	99	81.1	349	4 US-09-107-532A-6684	Sequence 6684, Ap
35	98	80.3	547	4 US-08-461-722-2	Sequence 2, Appl
36	98	80.3	547	4 US-08-336-251-2	Sequence 2, Appl
37	98	80.3	547	4 US-09-468-041-2	Sequence 2, Appl
38	98	80.3	547	5 PCT-US94-06362-2	Sequence 2, Appl
39	98	80.3	548	2 US-08-467-822-31	Sequence 31, Appl
40	98	80.3	548	2 US-08-467-822-32	Sequence 32, Appl
41	98	80.3	548	3 US-09-472-971-3	Sequence 3, Appl
42	98	80.3	548	3 US-08-432-697-31	Sequence 31, Appl
43	98	80.3	548	3 US-08-432-697-32	Sequence 32, Appl
44	98	80.3	548	3 US-08-466-248-31	Sequence 31, Appl
45	98	80.3	548	3 US-08-466-248-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-997-080-117
Sequence 117, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-117
Query Match 100.0%; Score 122; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKMGAPITINDG 22

DB 31 GPKGRNVLEKMGAPITINDG 52

RESULT 2

US-08-997-362-117

Sequence 117, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiwama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

TITLE OF INVENTION: PRESTIDGE, ROSE

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-117

Query Match 100.0%; Score 122; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 31 GPKGRNVLEKMGAPITINDG 52

RESULT 3

US-09-095-855-117

Sequence 117, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Rose

TITLE OF INVENTION: Compounds and Methods for

TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 29-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-095-855-117

Query Match 100.0%; Score 122; DB 3; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 31 GPKGRNVLEKMGAPITINDG 52

RESULT 4

US-09-324-542-117

Sequence 117, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul U.J.

APPLICANT: Prestidge, Rose

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 117

LENGTH: 215

TYPE: PRT

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 10.0741 Seconds
(without alignments)
152,738 Million cell updates/sec

Title: US-09-847-637b-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76: *
2: p1r1: *
3: p1r2: *
4: p1r3: *
5: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	90	100.0	A26950	groEL2 protein - M
2	90	100.0	A43509	65k antigen mbaA -
3	90	100.0	A41325	heat shock protein
4	90	100.0	S40245	heat shock protein
5	90	100.0	S41	chaperonin 60K [im
6	90	100.0	A25902	65k antigen - Myco
7	81	90.0	S70013	chaperonin-like pr
8	80	88.9	S73270	chaperonin, 60K
9	80	88.9	H72367	groEL protein, 60K
10	80	88.9	S41	chaperonin groEL -
11	80	88.9	S44	chaperonin groEL -
12	80	88.9	AG2263	chaperonin groEL (
13	79	87.8	S20876	chaperonin hsp60 p
14	78	86.7	S24	mitochondrial chap
15	77	85.6	S38	heat shock protein
16	77	85.6	S39	heat shock protein
17	77	85.6	S41	chaperonin groEL -
18	77	85.6	AC1704	class I heat-shock
19	77	85.6	AD1333	class I heat-shock
20	77	85.6	S43	heat shock protein
21	77	85.6	S43	chaperonin groEL,
22	77	85.6	S44	heat shock protein
23	77	85.6	S44	58k heat shock pro
24	77	85.6	JC6063	chaperonin groEL -
25	77	85.6	S44	class I heat-shock
26	76	84.4	S59	probable chaperoni
27	75	83.3	S40	heat shock protein
28	75	83.3	S41	chaperonin cpn60 -
29	75	83.3	S46	heat shock protein

ALIGNMENTS

RESULT 1

A26950 groEL2 protein - Mycobacterium tuberculosis (strain H37RV)

N/Alternate names: 65k antigen

C/Species: Mycobacterium tuberculosis

C/Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000

C/Accession: A26950, A70830

R/Shimnick, T.M.

J. Bacteriol. 169, 1080-1088, 1987

A/Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.

A/Reference number: A26950; MUID:87137260; PMID:3029018

A/Accession: A26950

A/Molecule type: DNA

A/Residues: 1-540 <SH1>

A/Cross-references: GB:M15467; NID:G149999; PIDN:AA88232.1; PID:G150000

R/Cole, S.T.; Brosch, K.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Comor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentile, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: A70830

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-540 <COL>

A/Cross-references: GB:AL021932; GB:AL123456; NID:G3261527; PIDN:CA17397.1; PID:G29095

A/Experimental source: strain H37RV

C/Genetics:

A/Gene: groEL2; RV0440

C/Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;

Best Local Similarity 100.0%; Pred. No. 5.2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVLEKKMGAP 16

Db 31 GPKGRNVLEKKMGAP 46

RESULT 2

A43509 65k antigen mbaA - Mycobacterium bovis

C/Species: Mycobacterium bovis

C/Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999

C/Accession: A43509

R/Thole, J.E.R.; Keulen, W.J.; Kolik, A.H.J.; Groothuis, D.G.; Berwald, L.G.; Tiesjema,

Infect. Immun. 55, 1466-1475, 1987

A/Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton

A/Reference number: A43509; MUID:8719315; PMID:3553003

A/Accession: A43509

chaperonin GroEL -

groEL protein - re

chaperonin groEL h

chaperonin groEL-2

chaperonin GroEL (

probable chaperoni

chaperonin Hsp60 -

heat shock protein

groEL protein - Ia

60 KD chaperonin (

heat shock protein

groEL - Brucella a

60k chaperonin gro

chaperonin, 60 kDa

60k heat shock pro

chaperonin 62.5k b

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <THO>
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKWGAP 16
|||
Db 31 GPKGRNVLEKKWGAP 46

RESULT 3

C41325
heat shock protein 56 - Streptomyces albus
N/Alternate names: heat shock protein groEL homolog 2
C/Species: Streptomyces albus
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 26-Aug-1999
C/Accession: C41325
R/Mazodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.
J. Bacteriol. 173, 7382-7386, 1991
A>Title: Characterization of the groEL-like genes in Streptomyces albus.
A/Reference number: A41325; PMID:92041639; PMID:1682304
A/Accession: C41325
A:Molecule type: DNA
A:Residues: 1-540 <MA2>
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294
C/Genetics:
A:Gene: groEL2
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKWGAP 16
|||
Db 31 GPKGRNVLEKKWGAP 46

RESULT 4

S40245
heat shock protein 65 - Mycobacterium paratuberculosis
C/Species: Mycobacterium paratuberculosis
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C/Accession: S40245
R/Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdosó, R.
submitted to the EMBL Data Library, August 1993
A/Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.
A/Reference number: S40245
A/Accession: S40245
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-541 <COL>
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKWGAP 16
|||
Db 31 GPKGRNVLEKKWGAP 46

RESULT 5

T44725
chaperonin 60K [imported] - Mycobacterium leprae
N/Alternate names: heat shock protein GroEL-2

C/Species: Mycobacterium leprae
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C/Accession: T44725
R/James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A/Reference number: Z22831
A/Accession: T44725
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-541 <JAM>
A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1
A/Experimental source: cosmid B1450
C/Genetics:
A:Gene: groEL-2
C:Superfamily: chaperonin groEL
C/Keywords: molecular chaperone

Query Match 100.0%; Score 90; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKWGAP 16
|||
Db 31 GPKGRNVLEKKWGAP 46

RESULT 6

A25902
65K antigen - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 12-Sep-1997
C/Accession: A25902
R/Mehra, V.; Sweetser, D.; Young, R.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986
A>Title: Efficient mapping of protein antigenic determinants.
A/Reference number: A25902; PMID:86313701; PMID:2428046
A/Accession: A25902
A:Molecule type: DNA
A:Residues: 1-588 <MEH>
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKWGAP 16
|||
Db 78 GPKGRNVLEKKWGAP 93

RESULT 7

S70013
chaperonin-like protein groEL2 - Synechococcus sp.
C/Species: Synechococcus sp.
C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 20-Jun-2000
C/Accession: S70013; S70022
R/Purki, M.; Tanaka, N.; Hiya, T.; Nakamoto, H.
Biochim. Biophys. Acta 1294, 106-110, 1996
A>Title: Cloning, characterization and functional analysis of groEL-like gene from the
A/Reference number: S70013; PMID:96248387; PMID:8645726
A/Accession: S70013
A:Molecule type: DNA
A:Residues: 1-543 <PUR>
A:Cross-references: GB:D86184; EMBL:D17354; NID:g1408522; PIDN:BA13082.1; PID:g1228065
A/Note: the source is designated as Synechococcus vulcanus
A:Molecule type: protein
A:Residues: 2-11 <PUR>
A/Note: the source is designated as Synechococcus vulcanus
C/Genetics:
A:Gene: groEL2
C:Superfamily: chaperonin groEL
C/Keywords: heat shock

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:08 ; Search time 6.81482 Seconds
(without alignments)
110.411 Million cell updates/sec

Title: US-09-847-637B-2
Sequence: 1 GPKGRNVLEKKGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	476	1	CH62_STRL1
2	90	100.0	539	1	CH60_TSUTY
3	90	100.0	539	1	CH62_MYCTU
4	90	100.0	539	1	CH62_STRL1
5	90	100.0	540	1	CH60_MYCPA
6	90	100.0	540	1	CH60_TSUPA
7	90	100.0	540	1	CH62_MYCLE
8	90	100.0	541	1	CH60_COREQ
9	90	100.0	541	1	CH60_NOCRA
10	90	100.0	541	1	CH62_STRCO
11	90	100.0	542	1	CH60_NOCAS
12	87	96.7	540	1	CH60_TROWT
13	85	94.4	541	1	CH60_PROAC
14	84	93.3	547	1	CH62_COREF
15	84	93.3	548	1	CH62_COREL
16	81	90.0	543	1	CH60_ANASL
17	81	90.0	543	1	CH62_SYNEL
18	80	88.9	300	1	CH60_SYNP6
19	80	88.9	528	1	CH60_PORPU
20	80	88.9	538	1	CH60_THENA
21	80	88.9	538	1	CH60_THENA
22	80	88.9	541	1	CH60_THENA
23	80	88.9	544	1	CH60_SYNP7
24	80	88.9	544	1	CH61_ANASP
25	80	88.9	544	1	CH61_SYNVU
26	80	88.9	543	1	CH60_SYNEL
27	79	87.8	543	1	CH60_BACFO
28	79	87.8	577	1	CH60_ARATH
29	78	86.7	529	1	CH60_GUITH
30	77	85.6	538	1	CH60_BACP3
31	77	85.6	539	1	CH60_BACST
32	77	85.6	539	1	CH60_BACTR
33	77	85.6	540	1	CH60_RHOMR

34	77	85.6	540	1	CH61_SYNV3	O05972 synechocyst
35	77	85.6	542	1	CH60_LISIN	Q923V0 listeria in
36	77	85.6	542	1	CH60_LISMO	Q9A966 listeria mo
37	77	85.6	543	1	CH60_BACSV	P28598 bacillus su
38	77	85.6	543	1	CH60_BACSV	O8R000 bacillus su
39	77	85.6	543	1	CH60_CLOAB	P30717 clostridium
40	77	85.6	544	1	CH60_BACCH	O50305 bacillus ha
41	76	84.4	530	1	CH60_CYACA	Q9L121 cyanidium c
42	76	84.4	543	1	CH60_IACJO	Q9K723 lactobacill
43	75	83.3	539	1	CH61_STRL1	O00767 streptomyce
44	75	83.3	540	1	CH61_STRL1	P40171 streptomyce
45	75	83.3	546	1	CH60_CHRY1	P31293 chromatiu

ALIGNMENTS

RESULT 1
ID CH62_STRL1 STANDARD; PRT; 476 AA.
AC O33658;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).
GN GROEL2 OR GROEL2.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=TK21;
RX MEDLINE=98048481; PubMed=9387235;
RA de Leon P, Marco S, Isiegas C, Marina A, Carrascosa J.L.,
RA Mellado R.P.;
RT "Streptomyces lividans groEL1 and groEL2 genes";
RL Microbiology 143:3563-3571(1997).
CC -1- FUNCTION: Prevents misfolding and promotes the refolding and
proper assembly of unfolded polypeptides generated under stress
conditions (By similarity).
CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
7 subunits (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sib-ch.ch).
CC
DR EMBL; X95971; CA65226.1; -.
DR HSSP; P06139; IGRL.
DR HAMAP; MF_00600; atypical; 1.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1; 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCF1.
DR PROSITE; PS00296; CHAPERONIN; Cpn60; 1.
KW Chaperone; ATP-binding; Multigene family.
FT INT MET 0
SQ SEQUENCE 476 AA; 50529 MW; 760F81793F4F5D4D CRC64;
Query Match 100.0%; Score 90; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKGAP 16
|||||

DB 30 GPKGRNVLEKKMGAP 45

RESULT 2

CH60_TSUTY STANDARD; PRT; 539 AA.

AC P97086;

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein 60).

GN GROEL OR GROEL OR HSP60.

OS *Taukamuraella tyrosinosolvens*.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; *Taukamuraella*.

OX NCBI_TaxID=57704;

XX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IMMB D-1411;

RA Zimmermann O., Pinkenburg O., Koehler H.G.;

RT "Taukamuraella tyrosinosolvens sp. nov. hsp60 gene for heat shock protein 60.";

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.

CC -----

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CC -----

CC EMBL; U90204; AAB49990.1; -.

DR HSP; P06139; IGR.

DR HAMAP; MF_00600; -; 1.

DR InterPro; IPR001844; Chaperon Cpn60.

DR InterPro; IPR002423; Cpn60/TCF-1.

DR Pfam; PF00118; Cpn60_TCF; 1.

DR PRINTS; PR00296; CHAPERONIN60.

DR PRINTS; PR00304; TCOMPLEXTCF.

DR PROSITE; PS00296; CHAPERONIN_CPN60; 1.

DR Chaperone; ATP-binding.

DR KW Chaperone; ATP-binding.

DR SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

SO

Query Match 100.0%; Score 90; DB 1; Length 539;

Best Local Similarity 100.0%; Pred. No. 6e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAP 16

DB 31 GPKGRNVLEKKMGAP 46

RESULT 3

CH62_MYCTU STANDARD; PRT; 539 AA.

AC P06806; Q48920; Q48931;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin 2 (Protein Cpn60-2) (groEL protein 2) (65 kDa anti-igen) (Heat shock protein 65) (Cell wall protein A) (Antigen A).

GN GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.

OS *Mycobacterium tuberculosis*, and *Mycobacterium bovis*.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; *Mycobacteriaceae*; *Mycobacterium*.

OX NCBI_TaxID=1773, 1765;

XX [1]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=Brdmann;

RX MEDLINE=87137260; PubMed=3029018;

RT Shinnick T.M.;

RL "The 65-kilodalton antigen of *Mycobacterium tuberculosis*.";

RL J. Bacteriol. 169:1080-1088 (1987).

XX [2]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=H37Rv;

RX MEDLINE=9825987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feldwell T., Gentile S., Hamlin S., Holroyd S., Hornby T., Jaffe K., Krogan A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence.";

RL Nature 393:537-544 (1998).

XX [3]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A., Bishai W.;

RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains.";

RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

XX [4]

RP SEQUENCE FROM N.A.

RC SPECIES=M.bovis; STRAIN=BCG;

RX MEDLINE=87193155; PubMed=3553003;

RA Thole J.E.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Berwald L.G., Tiesjema R.H., van Embden J.D.A.;

RT "Characterization, sequence determination, and immunogenicity of a 64-kilodalton protein of *Mycobacterium bovis* BCG expressed in *Escherichia coli* K-12.";

RL Infect. Immun. 55:1466-1475 (1987).

XX [5]

RP SEQUENCE OF 45-195 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, and 12-14001;

RA Ros C., Belak K.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

XX [6]

RP SEQUENCE OF 63-182 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TWC 410, and TWC 1024;

RX MEDLINE=95150784; PubMed=7848059;

RA Kapur V., Li L.L., Hamrick M.R., Plikaytis B.B., Shinnick T.M., Telenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y., Clarridge J.E., Kreiswirth B.N., Musser J.M.;

RT "Rapid *Mycobacterium* species assignment and unambiguous identification of mutations associated with antimicrobial resistance in *Mycobacterium tuberculosis* by automated DNA sequencing.";

RL Arch. Pathol. Lab. Med. 119:131-138 (1995).

XX [7]

RP SEQUENCE OF 64-177 FROM N.A.

RC SPECIES=M.tuberculosis;

RX MEDLINE=95214306; PubMed=7699930;

RA Hidaka E., Ueno I., Kawakami Y., Furutawari C., Furinata K., Katsuyama T.;

RT "Detection and identification of *Mycobacterium* by PCR-RFLP method.";

RL Rinsho Byori 43:155-161 (1995).

XX -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 25.7778 Seconds
(without alignments)
160.171 Million cell updates/sec

Title: US-09-847-637B-2
Perfect score: 90
Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	59	2	Q9EMD1 streptomyc
2	90	100.0	61	2	Q9EUR7 streptomyc
3	90	100.0	539	2	P97086 tsukamurell
4	90	100.0	540	2	Q9AFAS tsukamurell
5	90	100.0	541	2	Q93Q12 corynebacte
6	90	100.0	541	2	Q9AF66 nocardia fa
7	90	100.0	541	2	Q9KGM1 mycobacteri
8	90	100.0	542	2	Q9AFCS nocardia as
9	90	100.0	548	2	Q8GARS mycobacteri
10	90	100.0	548	2	Q8GAR7 mycobacteri
11	90	100.0	548	2	Q8G923 mycobacteri
12	90	100.0	548	2	Q8G8X0 mycobacteri
13	90	100.0	549	2	Q8GAR9 mycobacteri
14	85	94.4	533	2	Q9PDS2 propionibac
15	84	93.3	547	16	Q8CY22 corynebacte
16	84	93.3	548	16	Q8NM64 corynebacte

17	81	50.0	543	2	Q9AMJ8	Q9amj8 anabaena sp
18	80	88.9	545	16	Q8DMD4	Q8dmd4 synechococc
19	78	86.7	524	10	Q49314	Q49314 arabidopsis
20	78	86.7	585	10	Q8L7B5	Q8l7b5 arabidopsis
21	77	85.6	539	2	Q9EZV4	Q9ezv4 bacillus st
22	77	85.6	539	2	Q9RC20	Q9rc20 bacillus st
23	77	85.6	545	2	Q8GB95	Q8gb95 heliobacill
24	77	85.6	581	5	Q46219	Q46219 culicoides
25	76	84.4	598	5	Q9XYR7	Q9xyr7 onchocerca
26	76	84.4	599	10	P93570	P93570 solanum tub
27	75	83.3	546	2	Q31198	Q31198 leptospira
28	75	83.3	573	5	Q9USN2	Q9usn2 myzus persi
29	75	83.3	576	5	Q8WZB0	Q8wzb0 drosophila
30	75	83.3	576	5	Q8WZM9	Q8wzm9 trichinella
31	75	83.3	576	5	Q8IHD0	Q8ihd0 drosophila
32	75	83.3	580	5	Q96783	Q96783 plectus acu
33	75	83.3	582	5	Q9USL7	Q9usl7 paracentrot
34	74	82.2	543	2	Q8KZN2	Q8kzn2 thermus sp.
35	74	82.2	545	16	Q8CX13	Q8cx13 oceanobacil
36	73	81.1	174	10	P93571	P93571 solanum tub
37	73	81.1	531	2	Q8GBD0	Q8gbd0 enterococcu
38	73	81.1	531	2	Q8GBC6	Q8gbc6 enterococcu
39	73	81.1	531	2	Q8GBC4	Q8gbc4 enterococcu
40	73	81.1	531	2	Q8GBC2	Q8gbc2 enterococcu
41	73	81.1	531	2	Q8GBC0	Q8gbc0 enterococcu
42	73	81.1	532	2	Q8GBC8	Q8gbc8 enterococcu
43	73	81.1	532	2	Q8GBB8	Q8gbb8 enterococcu
44	73	81.1	532	16	Q8CWJ0	Q8cwj0 vibrio vuln
45	73	81.1	537	2	Q9K171	Q9k171 parascardov

ALIGNMENTS

RESULT 1

ID	Q9EMD1	PRELIMINARY	PRT	59 AA
AC	Q9EMD1			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Heat-shock protein (Fragment).			
GN	GROEL2			
OS	Streptomyces coelicolor.			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycinae; Streptomycetaceae; Streptomyces.			
OX	NCBI_TaxId=1902;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=J802;			
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.,			
RT	"A cold-shock-like gene with pleiotropic effects on Streptomyces			
RT	antibiotic biosynthesis."			
RT	Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ250536; CAC19351.1; -			
DR	HSSP; P06139; IACN.			
DR	InterPro; IPR002423; Cpn60/TCF-1.			
DR	Pfam; PF00118; cpn60 TCP1; 1.			
DR	PRINTS; PR00304; TCOMPLEXTCP1.			
KW	ATP-binding; Chaperone.			
FT	NON_TER			
SQ	SEQUENCE 59 AA; 6407 MW; E7B24199B7DB68FA CRC64;			
Query Match	100.0%; Score 90; DB 2; Length 59;			
Best Local Similarity	100.0%; Pred. No. 8e-08;			
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY 1 GPKGRNVLEKKMGAP 16
|||||
DB 31 GPKGRNVLEKKMGAP 46

RESULT 2

09EUR7 ID 09EUR7 PRELIMINARY; PRT; 61 AA.

AC 09EUR7;

DT 01-MAR-2001 (TREMBLREL. 16, Created)

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-MAR-2002 (TREMBLREL. 20, Last annotation update)

DE Heat-shock protein (Fragment).

GN GROEL2.

OS Streptomyces hygroscopicus.

OC Bacteria; Actinobacteria; Actinomycetales;

OC Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1912;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=AP 141;

RC Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.,

RT "A cold-shock-like gene with pleiotropic effects on Streptomyces

RT antibiotic biosynthesis."

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ250537; CAC19355.1; -.

DR HSSP; P06139; 1AON.

DR InterPro; IPR002423; Cpn60/TCP-1.

DR Pfam; PF00118; Cpn60 TCP1. 1.

DR PRINTS; PR00304; TCOMPLEXTCP1.

KM ATP-binding; Chaperone.

FT NCN TER 61

SQ SEQUENCE 61 AA; 6645 MW; D200995P4199B7CA CRC64;

Query Match 100.0%; Score 90; DB 2; Length 61;

Best Local Similarity 100.0%; Pred. No. 8.3e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPKGRNVLEKKGAP 16

Db 31 GPKGRNVLEKKGAP 46

RESULT 3

P97086 PRELIMINARY; PRT; 539 AA.

AC P97086;

DT 01-MAY-1997 (TREMBLREL. 03, Created)

DT 01-MAY-1997 (TREMBLREL. 03, Last sequence update)

DT 01-OCT-2002 (TREMBLREL. 22, Last annotation update)

DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL protein).

GN HSP60.

OS Tsukamurella tyrosinisolvens.

OC Bacteria; Actinobacteria; Actinomycetales;

OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.

OX NCBI_TaxID=57704;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=IMIB D-1411;

RC Zimmermann O., Pinkenburg O., Koechel H.G.,

RT "Tsukamurella tyrosinisolvens sp. nov. hsp60 gene for heat shock protein 60."

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

EMBL; U90204; AAB49990.1; -.

DR HSSP; P06139; 1GRL.

DR InterPro; IPR001844; Chaprin Cpn60.

DR InterPro; IPR002423; Cpn60/TCP-1.

DR Pfam; PF00118; Cpn60 TCP1. 1.

DR PRINTS; PR00298; CHAPERONIN60.

DR PRINTS; PR00304; TCOMPLEXTCP1.

DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.

KM ATP-binding; Chaperone.

SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BFTC CRC64;

Query Match 100.0%; Score 90; DB 2; Length 540;

Best Local Similarity 100.0%; Pred. No. 8.6e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPKGRNVLEKKGAP 16

Db 31 GPKGRNVLEKKGAP 46

RESULT 5

093012 PRELIMINARY; PRT; 541 AA.

AC 093012;

DT 01-DEC-2001 (TREMBLREL. 19, Created)

DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLREL. 23, Last annotation update)

DE groEL protein (60 kDa chaperonin) (Protein Cpn60).

GN GROEL.

OS Corynebacterium equi (Rhodococcus equi).

OC Bacteria; Actinobacteria; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=43767;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=ATCC6939;

RC Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match 100.0%; Score 90; DB 2; Length 539;

Best Local Similarity 100.0%; Pred. No. 8.5e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPKGRNVLEKKGAP 16

Db 31 GPKGRNVLEKKGAP 46

RESULT 4

09AFAS PRELIMINARY; PRT; 540 AA.

AC 09AFAS;

DT 01-JUN-2001 (TREMBLREL. 17, Created)

DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)

DT 01-OCT-2002 (TREMBLREL. 22, Last annotation update)

DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL protein).

GN HSP60.

OS Tsukamurella paurometabola.

OC Bacteria; Actinobacteria; Actinomycetales;

OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.

OX NCBI_TaxID=2061;

RN [1]

RP SEQUENCE FROM N.A.

RA Zimmermann O.S., Koechel H.G.,

RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

EMBL; AF352578; AAK18614.1; -.

DR HSSP; P06139; 1GRL.

DR InterPro; IPR001844; Chaprin Cpn60.

DR InterPro; IPR002423; Cpn60/TCP-1.

DR Pfam; PF00118; Cpn60 TCP1. 1.

DR PRINTS; PR00298; CHAPERONIN60.

DR PRINTS; PR00304; TCOMPLEXTCP1.

DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.

KM ATP-binding; Chaperone.

SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BFTC CRC64;

Query Match 100.0%; Score 90; DB 2; Length 540;

Best Local Similarity 100.0%; Pred. No. 8.6e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPKGRNVLEKKGAP 16

Db 31 GPKGRNVLEKKGAP 46

RESULT 5

093012 PRELIMINARY; PRT; 541 AA.

AC 093012;

DT 01-DEC-2001 (TREMBLREL. 19, Created)

DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLREL. 23, Last annotation update)

DE groEL protein (60 kDa chaperonin) (Protein Cpn60).

GN GROEL.

OS Corynebacterium equi (Rhodococcus equi).

OC Bacteria; Actinobacteria; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI_TaxID=43767;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=ATCC6939;

RC Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

M. vaccae GroEL hom
Amino acid sequenc
Sequence of Mycob
Mycobacterium tube
Mycobacteria sp. h
Mycobacterium tube
Amino acid sequenc
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Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
Amino acid sequenc
M. leprae 65KDa st
M. tuberculosis 65S
Mycobacterium lepra
Mycobacterium tube
Mycobacterium tube
M. leprae 65KDa st
M. tuberculosis 65S
M. leprae GroEL g
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
M. vaccae GroEL hom
Mycobacteria sp. h
Sequence of Mycob
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
M. leprae 65 KDa p
M. tuberculosis 65S
M. leprae 65Kd ant
Heat shock protein
Amino acid sequenc
Amino acid sequenc
BCG Hsp65/mutant H
BCG Hsp65/mutant H
BCG Hsp65/mutant H

1	90	100.0	16	21	AAV933329	Amino acid sequenc
2	90	100.0	16	21	AAU939964	Mycobacterium tube
3	90	100.0	22	21	AAV933328	Amino acid sequenc
4	90	100.0	215	19	AAAG60145	M. vaccae antigen
5	90	100.0	215	20	AA144832	Amino acid sequenc
6	90	100.0	215	23	ABR73438	M vaccae GroEL hom
7	90	100.0	225	22	AAAB31615	Amino acid sequenc
8	90	100.0	523	19	AAAG60144	M. vaccae antigen
9	90	100.0	523	20	AAV14891	Amino acid sequenc

10	90	100.0	523	23	AB873497.9
11	90	100.0	539	20	AA873391.9
12	90	100.0	540	9	AA8781351
13	90	100.0	540	16	AA8781610
14	90	100.0	540	10	AA8721000
15	90	100.0	540	19	AA8747022
16	90	100.0	540	20	AA873391.1
17	90	100.0	540	21	AA8733322
18	90	100.0	540	22	AA8717555
19	90	100.0	540	22	AA8781118
20	90	100.0	540	22	AA8781606
21	90	100.0	540	23	AA8765100
22	90	100.0	540	23	AA87651.1
23	90	100.0	540	23	AA8761933
24	90	100.0	540	23	AA876194
25	90	100.0	540	23	AA8507504
26	90	100.0	540	24	AB8745878
27	90	100.0	540	24	AB8745888
28	90	100.0	541	16	AA8673844
29	90	100.0	541	20	AA8749009
30	90	100.0	541	20	AA8733910
31	90	100.0	541	20	AA8733913
32	90	100.0	541	23	AB8735155
33	90	100.0	544	18	AA8720099
34	90	100.0	550	9	AA8780215
35	90	100.0	572	11	AA8747176
36	90	100.0	573	11	AA8747175
37	90	100.0	573	16	AA8747655
38	90	100.0	573	16	AA8747656
39	90	100.0	588	9	AA8780364
40	90	100.0	638	21	AA8703790
41	90	100.0	639	22	AA8716099
42	90	100.0	648	22	AA8716144
43	90	100.0	690	23	AB8707777
44	90	100.0	709	23	AB8707766
45	90	100.0	724	23	AB8707778

M. vaccae GroEL hom
Amino acid sequenc
Sequence of Mycob
Mycobacterium tube
Mycobacteria sp. h
Mycobacterium tube
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Amino acid sequenc
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Amino acid sequenc
M. leprae 65KDa st
M. tuberculosis 65S
Mycobacterium lepra
Mycobacterium tube
Mycobacterium tube
M. leprae 65KDa st
M. tuberculosis 65S
M. leprae GroEL g
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
M. vaccae GroEL hom
Mycobacteria sp. h
Sequence of Mycob
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
M. leprae 65 KDa p
M. tuberculosis 65S
M. leprae 65Kd ant
Heat shock protein
Amino acid sequenc
Amino acid sequenc
BCG Hsp65/mutant H
BCG Hsp65/mutant H
BCG Hsp65/mutant H

XX	RESULT 1
XX	AA993329
ID	AA993329 standard; peptide; 16 AA.
XX	
AC	AA993329; ,
XX	
DT	04-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of an epitope of heat shock protein 60.
XX	
XX	Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KW	inflammatory disorder; arthritis.
XX	
OS	Mycobacterium tuberculosis.
XX	
FN	WC200027870-A1.
XX	
PD	18-MAY-2000.
XX	
PF	04-NOV-1999; 99WO-IL00595.
XX	
PR	05-NOV-1998; 98US-0107213.
XX	
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX	
PI	Naparstek Y, Ulmansky R, Kashi Y;
XX	
DR	WPI; 2000-376486/32.
XX	
PT	Peptide having a defined sequence is used in vaccines for conferring
XX	immunity against autoimmune disease or inflammatory disorders,
XX	especially arthritis -

XX Claim 2; Page 7; 58pp; English.
 PS
 CC The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 90; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVLEKKWGAP 16
 DB 1 GPKGRNVLEKKWGAP 16
 RESULT 2
 ID AAU99964 standard; Peptide; 16 AA.
 AC AAU99964;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.
 XX
 KM Heat shock protein; hsp; hsp60; chronic inflammatory disease;
 KM autoimmune disease; infectious disease; graft rejection; type 1 diabetes;
 KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
 KM systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
 KM arteriosclerosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200248312-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 11-DEC-2001; 2001WO-IL01144.
 XX
 PR 11-DEC-2000; 2000IL-0140233.
 XX
 PA (PEPT-) PEPTOR LTD.
 XX
 PI Bias D, Avron A, Senderowitz H;
 XX
 DR WPI; 2002-557613/59.
 XX
 PT New backbone cyclised peptide analog of heat shock protein useful in
 PT the treatment of e.g. autoimmune disease
 XX
 PS Claim 5; Page 42; 50pp; English.
 XX
 CC The invention relates to backbone cyclised peptide analogues or
 CC antagonists of heat shock protein (hsp). The analogues and antagonists
 CC are useful in the treatment of chronic inflammatory disease, autoimmune
 CC disease, infectious disease and graft rejection, and for diagnosing
 CC autoimmune and inflammatory disease including juvenile rheumatoid
 CC arthritis, type 1 diabetes, multiple sclerosis, systemic lupus
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide
 CC analogue of a heat shock protein.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 90; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16
 DB 1 GPKGRNVLEKKWGAP 16
 RESULT 3
 ID AAY93328 standard; peptide; 22 AA.
 AC AAY93328;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of an epitope of heat shock protein 60.
 XX
 KM Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
 KM inflammatory disorder; arthritis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200027870-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 04-NOV-1999; 99WO-IL00595.
 XX
 PR 05-NOV-1998; 98US-0107213.
 XX
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 XX
 PI Naparsatek Y, Umanaky R, Kashi Y;
 XX
 DR WPI; 2000-376486/32.
 XX
 PT Peptide having a defined sequence is used in vaccines for conferring
 PT immunity against autoimmune disease or inflammatory disorders,
 PT especially arthritis
 XX
 PS Claim 1; Page 7; 58pp; English.
 XX
 CC The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX
 SQ Sequence 22 AA;
 Query Match 100.0%; Score 90; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVLEKKWGAP 16
 DB 1 GPKGRNVLEKKWGAP 16
 RESULT 4
 ID AAW60145 standard; Protein; 215 AA.
 AC AAW60145;
 XX
 DT 25-AUG-1998 (first entry)
 XX
 DE M. vaccae antigen GV-27A sequence.
 XX
 KM Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
 KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
 KM mycobacteria infection; vaccine; cancer.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:09:39 : Search time 21.9259 Seconds
(without alignments)
145.229 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVYLEKKWGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	10	US-09-847-637B-2
2	90	100.0	22	10	US-09-847-637B-1
3	90	100.0	215	11	US-09-880-505-117
4	90	100.0	215	12	US-10-205-979-41
5	90	100.0	215	14	US-10-051-643-117
6	90	100.0	295	15	US-10-267-311-33
7	90	100.0	523	11	US-09-880-505-114
8	90	100.0	523	14	US-10-051-643-114
9	90	100.0	540	10	US-09-847-637B-6
10	90	100.0	540	15	US-09-712-363-169
11	90	100.0	540	15	US-10-267-311-4
12	90	100.0	540	15	US-10-046-649-3
13	90	100.0	540	15	US-10-046-649-4
14	90	100.0	541	11	US-09-880-505-160
15	90	100.0	541	12	US-10-205-979-40

16	90	100.0	541	14	US-10-051-643-160	Sequence 160, App
17	90	100.0	541	15	US-10-156-761-11465	Sequence 11465, A
18	90	100.0	576	12	US-10-369-493-8322	Sequence 8322, Ap
19	90	100.0	639	15	US-10-267-311-17	Sequence 17, Appl
20	90	100.0	648	15	US-10-267-311-29	Sequence 29, Appl
21	90	100.0	690	14	US-10-068-059-10	Sequence 10, Appl
22	90	100.0	709	14	US-10-068-059-8	Sequence 8, Appl
23	90	100.0	724	14	US-10-068-059-12	Sequence 12, Appl
24	90	100.0	746	14	US-10-068-059-6	Sequence 6, Appl
25	90	100.0	948	15	US-10-267-311-21	Sequence 21, Appl
26	84	93.3	548	10	US-09-738-626-6486	Sequence 6486, Ap
27	82	91.1	547	12	US-10-369-493-10014	Sequence 10014, A
28	80	88.9	538	12	US-10-369-493-2950	Sequence 2950, Ap
29	80	88.9	544	12	US-10-369-493-20276	Sequence 20276, A
30	80	88.9	544	12	US-10-369-493-20873	Sequence 20873, A
31	79	87.8	545	12	US-10-369-493-19756	Sequence 19756, A
32	77	85.6	544	12	US-10-369-493-17132	Sequence 17132, A
33	77	85.6	544	12	US-10-369-493-23094	Sequence 23094, A
34	77	85.6	551	12	US-10-369-493-20184	Sequence 20184, A
35	75	83.3	521	12	US-10-369-493-9597	Sequence 9597, Ap
36	75	83.3	540	12	US-10-369-493-15838	Sequence 15838, A
37	75	83.3	542	15	US-10-156-761-12526	Sequence 12526, A
38	75	83.3	544	12	US-10-369-493-15468	Sequence 15468, A
39	75	83.3	544	12	US-10-369-493-16217	Sequence 16217, A
40	74	82.2	551	12	US-10-369-493-18994	Sequence 18994, A
41	74	82.2	552	12	US-10-369-493-2799	Sequence 2799, Ap
42	73	81.1	547	12	US-10-369-493-10235	Sequence 10235, A
43	72	80.0	547	15	US-10-046-649-2	Sequence 2, Appl
44	72	80.0	548	11	US-09-415-849-1	Sequence 1, Appl
45	72	80.0	548	11	US-09-276-455-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-847-637B-2
; Sequence 2, Application US/09847637B
; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Umanetsky, Rina
; APPLICANT: Kasht, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-2
Query Match 100.0%; Score 90; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVYLEKKWGAP 16
DB 1 GPKGRNVYLEKKWGAP 16
RESULT 2
US-09-847-637B-1
; Sequence 1, Application US/09847637B

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; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Naparstek, Rina
; APPLICANT: Ulimansky, Rina
; APPLICANT: Kasbi, Yecheskel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-09-847-637B-1

Query Match      100.0%; Score 90; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      1 GPKGRNVVLEKKWGAP 16

RESULT 3
US-09-880-505-117
; Sequence 117, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-09-880-505-117

Query Match      100.0%; Score 90; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      31 GPKGRNVVLEKKWGAP 46

RESULT 4
US-10-205-979-41
; Sequence 41, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.

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; APPLICANT: Abernethy, Nevlin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-10-205-979-41

Query Match      100.0%; Score 90; DB 12; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      31 GPKGRNVVLEKKWGAP 46

RESULT 5
US-10-051-643-117
; Sequence 117, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-10-051-643-117

Query Match      100.0%; Score 90; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPKGRNVVLEKKWGAP 16
DB      31 GPKGRNVVLEKKWGAP 46

RESULT 6
US-10-267-311-33
; Sequence 33, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10

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GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: December 30, 2003, 16:06:09 / Search time 11.2593 Seconds
(without alignments)
60.126 Million cell updates/sec

Title: US-09-847-637B-2
Perfect score: 90
Sequence: 1 GPKGRNVLEKKWGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.rep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.rep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.rep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.rep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.rep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.rep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	90	100.0	215 2 US-08-997-080-117	Sequence 117, App
2	90	100.0	215 2 US-08-997-362-117	Sequence 117, App
3	90	100.0	215 3 US-09-095-855-117	Sequence 117, App
4	90	100.0	215 4 US-09-324-542-117	Sequence 117, App
5	90	100.0	215 4 US-09-205-426-117	Sequence 117, App
6	90	100.0	295 4 US-09-613-303-33	Sequence 33, App
7	90	100.0	523 2 US-08-997-080-114	Sequence 114, App
8	90	100.0	523 2 US-08-997-362-114	Sequence 114, App
9	90	100.0	523 3 US-09-095-855-114	Sequence 114, App
10	90	100.0	523 4 US-09-324-542-114	Sequence 114, App
11	90	100.0	523 4 US-09-205-426-114	Sequence 114, App
12	90	100.0	540 2 US-08-368-834-20	Sequence 20, App
13	90	100.0	540 4 US-08-461-722-3	Sequence 3, App
14	90	100.0	540 4 US-08-461-722-4	Sequence 3, App
15	90	100.0	540 4 US-08-336-251-3	Sequence 3, App
16	90	100.0	540 4 US-08-336-251-4	Sequence 3, App
17	90	100.0	540 4 US-09-468-041-3	Sequence 3, App
18	90	100.0	540 4 US-09-468-041-4	Sequence 3, App
19	90	100.0	540 4 US-09-613-303-4	Sequence 4, App
20	90	100.0	540 5 PCT-US94-06362-3	Sequence 3, App
21	90	100.0	540 5 PCT-US94-06362-4	Sequence 3, App
22	90	100.0	541 2 US-08-467-822-34	Sequence 34, App
23	90	100.0	541 2 US-08-447-154-19	Sequence 19, App
24	90	100.0	541 2 US-08-997-080-160	Sequence 160, App
25	90	100.0	541 2 US-08-997-362-160	Sequence 160, App
26	90	100.0	541 3 US-09-095-855-160	Sequence 160, App
27	90	100.0	541 3 US-08-432-697-34	Sequence 34, App

28	90	100.0	541 3 US-08-466-248-34	Sequence 34, App
29	90	100.0	541 4 US-09-324-542-160	Sequence 160, App
30	90	100.0	541 4 US-09-205-426-160	Sequence 160, App
31	90	100.0	639 4 US-09-613-303-17	Sequence 17, App
32	90	100.0	648 4 US-09-613-303-29	Sequence 29, App
33	90	100.0	948 4 US-09-613-303-21	Sequence 21, App
34	73	81.1	349 4 US-09-107-532A-6684	Sequence 6684, App
35	73	81.1	548 2 US-08-467-822-31	Sequence 31, App
36	73	81.1	548 3 US-08-432-697-31	Sequence 31, App
37	73	81.1	548 3 US-08-466-248-31	Sequence 31, App
38	72	80.0	547 4 US-08-461-722-2	Sequence 2, App
39	72	80.0	547 4 US-08-336-251-2	Sequence 2, App
40	72	80.0	547 4 US-09-468-041-2	Sequence 2, App
41	72	80.0	547 5 PCT-US94-06362-2	Sequence 2, App
42	72	80.0	548 2 US-08-467-822-32	Sequence 32, App
43	72	80.0	548 3 US-08-472-971-3	Sequence 3, App
44	72	80.0	548 3 US-08-432-697-32	Sequence 32, App
45	72	80.0	548 3 US-08-466-248-32	Sequence 32, App

ALIGNMENTS

RESULT 1
US-08-997-080-117
Sequence 117, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-117
Query Match 100.0%; Score 90; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 6, 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAP 16

Db 31 GPKGRNVLEKKMGAP 46

RESULT 2

US-08-997-362-117
Sequence 117, Application US/08997362

GENERAL INFORMATION:

APPLICANT: Tan, Paul
APPLICANT: Hiayama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-117

Query Match 100.0%; Score 90; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 6,1e-08; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0;

Db 31 GPKGRNVLEKKMGAP 46

RESULT 3

US-09-095-855-117
Sequence 117, Application US/09095855

GENERAL INFORMATION:

APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-117

Query Match 100.0%; Score 90; DB 3; Length 215;

Best Local Similarity 100.0%; Pred. No. 6,1e-08; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0;

Db 31 GPKGRNVLEKKMGAP 46

RESULT 4

US-09-324-542-117
Sequence 117, Application US/09324542

GENERAL INFORMATION:

APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 117
LENGTH: 215
TYPE: PRT

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 10.0741 Seconds
(without alignments)
152.738 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKRWGAPITINDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	87	100.0	540 2 A26950	groEL2 protein - M
2	87	100.0	540 2 A43509	65K antigen mbaA -
3	87	100.0	540 2 A41325	heat shock protein
4	87	100.0	541 2 S40245	heat shock protein
5	87	100.0	541 2 T44725	chaperonin 60K (Im
6	87	100.0	588 2 A25902	65K antigen - Myco
7	77	88.5	538 2 H72367	groEL protein - Th
8	72	82.8	540 2 S37566	groEL2 protein - S
9	72	82.8	540 2 B41325	heat shock protein
10	72	82.8	541 2 T35591	chaperonin cpn60 -
11	71	81.6	541 2 S72614	chaperonin 60 - Th
12	68	78.2	538 2 JQ1195	heat shock protein
13	68	78.2	539 2 B49855	heat shock protein
14	68	78.2	542 2 A21333	class I heat-shock
15	68	78.2	542 2 A21333	class I heat-shock
16	68	78.2	543 2 B41872	heat shock protein
17	68	78.2	543 2 F97232	chaperonin GroEL,
18	68	78.2	544 2 JCS130	heat shock protein
19	68	78.2	544 2 B41884	58K heat shock pro
20	68	78.2	544 2 JCS603	chaperonin groEL -
21	68	78.2	544 2 B83720	class I heat-shock
22	67	77.0	543 2 S70013	chaperonin-like pr
23	66	75.9	528 2 S73270	chaperonin, 60K -
24	66	75.9	541 2 T06829	chaperonin groEL
25	66	75.9	544 2 AG2263	chaperonin GroEL
26	66	75.9	546 2 S34938	heat shock protein
27	66	75.9	548 2 G75499	groEL protein - De
28	66	75.9	550 2 A41468	60K heat shock pro
29	65	74.7	541 2 S68249	chaperonin groEL h

30	65	74.7	544 1 BVCGL	chaperonin groEL -
31	65	74.7	546 2 B47073	chaperonin groEL -
32	64	73.6	535 2 JCS7858	GroEL protein - Te
33	64	73.6	539 2 S22342	chaperonin HSP60 -
34	64	73.6	542 2 JN0661	heat shock protein
35	64	73.6	542 2 S32106	groEL protein - La
36	64	73.6	542 2 B86574	60 KD chaperonin
37	63	72.4	540 2 G95222	chaperonin, 60 kDa
38	63	72.4	540 2 H98086	chaperonin GroEL
39	63	72.4	544 2 B82048	chaperonin, 60 kDa
40	63	72.4	547 2 JCS4519	heat-shock protein
41	63	72.4	547 2 B43606	heat shock protein
42	63	72.4	547 2 B89203	heat shock protein
43	63	72.4	547 2 B83098	groEL protein PA43
44	63	72.4	548 1 BVCGL	chaperonin groEL -
45	63	72.4	548 2 D91269	chaperonin GroEL

ALIGNMENTS

RESULT 1
A26950
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
N/Alternate names: 65K antigen
C/Species: Mycobacterium tuberculosis
C/Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000
C/Accession: A26950; A70830
R/Shimnick, T.M.
J. Bacteriol. 169, 1080-1088, 1987
A/Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.
A/Reference number: A26950; MUID:87137260; PMID:3029018
A/Accession: A26950
A/Molecule type: DNA
A/Residues: 1-540 <SH1>
A/Cross-references: GB:M5467; NID:g149999; PIDN:AA88232.1; PID:g150000
R/Comor, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Cole, S.T.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulterson, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:96295987; PMID:9634230
A/Accession: A70830
A/Status: Preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-540 <COL>
A/Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CA17397.1; PID:g29095
C/Genetic: A70830
A/Experimental source: strain H37RV
A/Accession: A70830
C/Suprafamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VVLEKRWGAPITINDG 16
DB 37 VVLEKRWGAPITINDG 52

RESULT 2
A43509
65K antigen mbaA - Mycobacterium bovis
C/Species: Mycobacterium bovis
C/Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C/Accession: A43509
R/Thole, J.E.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Berwald, L.G.; Tiesjema, I.
Infect. Immun. 55, 1466-1475, 1987
A/Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton
A/Reference number: A43509; MUID:87193155; PMID:3553003
A/Accession: A43509

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <THO>
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16
|||
Db 37 VVLEKKMGAPTTNDG 52

RESULT 3

C41325
heat shock protein 56 - Streptomyces albus
N:Alternate names: heat shock protein groEL homolog 2
C:Species: Streptomyces albus
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 26-Aug-1999
C:Accession: C41325
R:Maizodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.
J. Bacteriol. 173, 7382-7386, 1991
A:Title: Characterization of the groEL-like genes in Streptomyces albus.
A:Reference number: A41325; MUID:92041639; PMID:1682304
A:Accession: C41325
A:Molecule type: DNA
A:Residues: 1-540 <MAZ>
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294
C:Genetics:
A:Gene: groEL2
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16
|||
Db 37 VVLEKKMGAPTTNDG 52

RESULT 4

S40245
heat shock protein 65 - Mycobacterium paratuberculosis
C:Species: Mycobacterium paratuberculosis
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S40245
R:Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdosó, R.
submitted to the EMBL Data Library, August 1993
A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65MD.
A:Reference number: S40245
A:Accession: S40245
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-541 <COL>
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16
|||
Db 37 VVLEKKMGAPTTNDG 52

RESULT 7
H72367
groEL protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: H72367
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <ARN>
A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:ADJ35591.1; PID:g49810
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0506
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16
|||
Db 37 VVLEKKMGAPTTNDG 52

RESULT 5
T44725
chaperonin 60K [imported] - Mycobacterium leprae
N:Alternate names: heat shock protein GroEL-2

C:Species: Mycobacterium leprae
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T44725
R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z22831
A:Accession: T44725
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-541 <JAM>
A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1
A:Experimental source: cosmid B1450
C:Genetics:
A:Gene: groEL-2
C:Superfamily: chaperonin groEL
C:Keywords: molecular chaperone

Query Match 100.0%; Score 87; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16
|||
Db 37 VVLEKKMGAPTTNDG 52

RESULT 6
A25902
65K antigen - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 12-Sep-1997
C:Accession: A25902
R:Mehta, V.; Sweetser, D.; Young, R.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986
A:Title: Efficient mapping of protein antigenic determinants.
A:Reference number: A25902; MUID:86313701; PMID:2428046
A:Accession: A25902
A:Molecule type: DNA
A:Residues: 1-588 <MEH>
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16
|||
Db 84 VVLEKKMGAPTTNDG 99

RESULT 7
H72367
groEL protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: H72367
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <ARN>
A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:ADJ35591.1; PID:g49810
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0506
C:Superfamily: chaperonin groEL

Query Match 88.5%; Score 77; DB 2; Length 538;

DB 36 VLEKKMGAPTTNDG 51

RESULT 2

CH60_TSUTY STANDARD; PRT; 539 AA.

AC P97086; 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (heat shock protein 60).

GN GROEL OR GROEL OR HSP60.

OS *Taukamuraella tyrosinoseolvens*.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; *Taukamuraellaceae*; *Taukamuraella*.

OX NCBI_TaxID=57704;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IMW18 D-1411;

RA Zimmermann O., Pinkenburg O., Koehnel H.G.;

RT "Taukamuraella tyrosinoseolvens sp. nov. hsp60 gene for heat shock protein 60."

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of 7 subunits (By similarity).

CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.

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CC -----

DR EMBL: U90204; AABA9990.1; -

DR HSP60; P06139; 1GRU.

DR HAMAP: MF_00600; -; 1.

DR InterPro: IPR001844; Chaperonin Cpn60.

DR InterPro: IPR002423; Cpn60/TCF-1.

DR Pfam: PF00118; Cpn60 TCF; 1.

DR PRINTS: PRO0298; CHAPERONIN60.

DR PRINTS: PRO0304; TCOMPLEXTCP.

DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.

DR Chaperone; ATP-binding.

DR KW SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

SO

Query Match 100.0%; Score 87; DB 1; Length 539;

Best Local Similarity 100.0%; Pred. No. 4.5e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTNDG 16

DB 37 VLEKKMGAPTTNDG 52

RESULT 3

CH62_MYCTU STANDARD; PRT; 539 AA.

AC P06806; Q48920; Q48931;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 60 kDa chaperonin 2 (protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (heat shock protein 65) (Cell wall protein A) (Antigen A).

GN GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.

OS *Mycobacterium tuberculosis*, and *Mycobacterium bovis*.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; *Mycobacteriaceae*; *Mycobacterium*.

OX NCBI_TaxID=1773, 1765;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=Erasmus;

RX MEDLINE=87137260; PubMed=3029018;

RA Shinnick T.M.;

RT "The 65-kilodalton antigen of *Mycobacterium tuberculosis*."

RL J. Bacteriol. 169:1080-1088(1987).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=H37Rv;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagsle K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulten J.E., Taylor K., Whitehead S., Barrell B.G.;

RA "Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence."

RL Nature 393:537-544(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey B., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A., Bishai W.;

RA "Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains."

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=M.bovis; STRAIN=BCG;

RX MEDLINE=87193155; PubMed=3553003;

RA Thole J.E.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Berwald L.G., Tiesjema R.H., van Embden J.D.A.;

RA "Characterization, sequence determination, and immunogenicity of a 64-kilodalton protein of *Mycobacterium bovis* BCG expressed in *Escherichia coli* K-12."

RL Infect. Immun. 55:1466-1475(1987).

RN [5]

RP SEQUENCE OF 45-195 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, and 12-14001;

RA Ros C., Belak K.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE OF 63-182 FROM N.A.

RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TWC 410, and TWC 1024;

RX MEDLINE=95150784; PubMed=7848059;

RA Kapur V., Li L.L., Hamrick M.R., Plikaytis B.B., Shinnick T.M., Telenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y., Claridge J.E., Kreiswirth B.N., Musser J.M.;

RA "Rapid *Mycobacterium* species assignment and unambiguous identification of mutations associated with antitubercular resistance in *Mycobacterium tuberculosis* by automated DNA sequencing."

RL Arch. Pathol. Lab. Med. 119:131-138(1995).

RN [7]

RP SEQUENCE OF 64-177 FROM N.A.

RC SPECIES=M.tuberculosis;

RX MEDLINE=95214306; PubMed=7699930;

RA Hatake E., Ueno I., Kawakami Y., Furutani C., Furuhata K., Katsuyama T.;

RA "Detection and identification of *Mycobacterium* by PCR-RFLP method."

RL Rinsho Byori 43:115-161(1995).

CC -1- FUNCTION: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions (By similarity).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 25.7778 Seconds
(without alignments)
160.171 Million cell updates/sec

Title: US-09-847-637B-3
Perfect score: 87
Sequence: 1 VLEKMGAPITNDG 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	59	2	Q9BWD1 streptomyc
2	87	100.0	61	2	Q9BWD1 streptomyc
3	87	100.0	539	2	P97086 tsukamureli
4	87	100.0	540	2	Q9AFAS tsukamureli
5	87	100.0	541	2	Q93Q12 corynebacte
6	87	100.0	541	2	Q9APAG corynebacte
7	87	100.0	541	2	Q9KGM1 corynebacte
8	87	100.0	542	2	Q9APCS corynebacte
9	87	100.0	548	2	Q9BWD1 streptomyc
10	87	100.0	548	2	Q9BWD1 streptomyc
11	87	100.0	548	2	Q9BWD1 streptomyc
12	87	100.0	548	2	Q9BWD1 streptomyc
13	87	100.0	549	2	Q9BWD1 streptomyc
14	87	100.0	549	2	Q9BWD1 streptomyc
15	87	100.0	549	2	Q9BWD1 streptomyc
16	87	100.0	549	2	Q9BWD1 streptomyc

17	70	80.5	537	2	Q9K171 parascardov
18	70	80.5	541	2	Q9K157 gaidnerella
19	69	79.3	537	2	Q9BWD1 streptomyc
20	69	79.3	538	2	Q9BWD1 streptomyc
21	69	79.3	541	16	Q9B879 scardovia i
22	69	79.3	582	2	Q9B879 scardovia i
23	68	78.2	539	2	Q9B879 scardovia i
24	68	78.2	539	2	Q9B879 scardovia i
25	68	78.2	543	2	Q9B879 scardovia i
26	68	78.2	543	2	Q9B879 scardovia i
27	67	77.0	539	2	Q9B879 scardovia i
28	67	77.0	543	2	Q9B879 scardovia i
29	66	75.9	352	2	Q9B879 scardovia i
30	66	75.9	545	16	Q9B879 scardovia i
31	66	75.9	546	2	Q9B879 scardovia i
32	65	74.7	545	16	Q9B879 scardovia i
33	64	73.6	531	2	Q9B879 scardovia i
34	64	73.6	531	2	Q9B879 scardovia i
35	64	73.6	531	2	Q9B879 scardovia i
36	64	73.6	531	2	Q9B879 scardovia i
37	64	73.6	531	2	Q9B879 scardovia i
38	64	73.6	532	2	Q9B879 scardovia i
39	64	73.6	532	2	Q9B879 scardovia i
40	63	72.4	82	2	Q9B879 scardovia i
41	63	72.4	191	2	Q9B879 scardovia i
42	63	72.4	329	2	Q9B879 scardovia i
43	63	72.4	329	2	Q9B879 scardovia i
44	63	72.4	329	2	Q9B879 scardovia i
45	63	72.4	329	2	Q9B879 scardovia i

ALIGNMENTS

Q9BWD1	PRELIMINARY;	PRT;	59 AA.
AC Q9BWD1	01-MAR-2001 (TREMBLrel. 16, Created)		
DT 01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT 01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	Heat-shock protein (Fragment)		
GN	GROEL2.		
OS	Streptomyces coelicolor.		
OC	Bacteria; Actinobacteridae; Actinomycetales;		
OC	Streptomycinae; Streptomycetaceae; Streptomyces.		
OX	NCBI_TaxID=1902;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=J802;		
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;		
RT	"A cold-shock-like gene with pleiotropic effects on Streptomyces		
RT	antibiotic biosynthesis."		
RL	Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ250536; CAC19351.1; .		
DR	HSSP; P06139; 1AON.		
DR	InterPro; IPR002423; Cpn60/TCF-1.		
DR	Pfam; PF00118; cpn60 TCPL; 1.		
KW	PRINTS; PR00304; TCOMPLEXTCPL.		
FT	ATP-binding; Chaperone.		
FT	NON_TER		
FT	SEQUENCE 59 AA; 6407 MW; E7B24199B7DB68FA CRC64;		
Q9	1 VLEKMGAPITNDG 16		
DB	37 VLEKMGAPITNDG 52		
RESULT 2			

```

Q9EUR7 PRELIMINARY; PRT; 61 AA.
ID Q9EUR7
AC Q9EUR7;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Heat-shock protein (Fragment).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OK NCBI_TaxId=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
antibiotic biosynthesis."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250537; CAC19355.1; -.
DR HSSP; P06139; 1AON.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1.1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
KW ATP-binding; Chaperone.
FT NON TER 61
SQ SEQUENCE 61 AA; 6645 MW; D20095F419B7CA CRC64;

Query Match 100.0%; Score 87; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 3
P97086 PRELIMINARY; PRT; 539 AA.
ID P97086
AC P97086;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
protein).
GN HSP60.
OS Tsukamurella tyrosinosolvens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OK NCBI_TaxId=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMTB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
protein 60."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RT FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DE EMBL; U90204; AAB49990.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00236; CHAPERONIN_CPN60.1.
KW ATP-binding; Chaperone.
FT
SQ SEQUENCE 540 AA; 56506 MW; 52485CDB2C49BF7C CRC64;

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 5
Q93012 PRELIMINARY; PRT; 541 AA.
ID Q93012
AC Q93012;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OK NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

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SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match 100.0%; Score 87; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 4
Q9AFAS PRELIMINARY; PRT; 540 AA.
ID Q9AFAS
AC Q9AFAS;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60) (groEL
protein).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OK NCBI_TaxId=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DE EMBL; AF32578; AKI18614.1; -.
DR HSSP; P06139; 1GRL.
DR InterPro; IPR001844; Chaperin Cpn60.
DR InterPro; IPR002423; Cpn60/TCF-1.
DR Pfam; PF00118; Cpn60_TCF1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00236; CHAPERONIN_CPN60.1.
KW ATP-binding; Chaperone.
FT
SQ SEQUENCE 540 AA; 56506 MW; 52485CDB2C49BF7C CRC64;

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKKGAPTTNDG 16
Db 37 VLEKKKGAPTTNDG 52

RESULT 5
Q93012 PRELIMINARY; PRT; 541 AA.
ID Q93012
AC Q93012;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE groEL protein (60 kDa chaperonin) (Protein Cpn60).
GN GROEL.
OS Corynebacterium equi (Rhodococcus equi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OK NCBI_TaxId=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6939;
RA Vanniasinkam T., Barton M.D., Heuzenroeder M.W.;

```



```

XX PS Claim 3; Page 7; 58pp; English.
XX CC The present sequence represents an epitope of the heat shock protein
XX CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
XX CC nucleic acid encoding it, are useful in vaccines for conferring
XX CC immunity against autoimmune disease or inflammatory disorders,
XX CC especially arthritis. The peptide may also be used to raise
XX CC antibodies, which are then used for passive immunisation.
XX SQ Sequence 16 AA;

Query Match 100.0%; Score 87; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKWGAPITNDG 16
DB 1 VVLEKKWGAPITNDG 16

RESULT 2
AAU99965
ID AAU99965 standard; Peptide; 16 AA.
AC AAU99965;
XX
XX 07-OCT-2002 (first entry)
XX
XX Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.
XX
XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;
XX KM autoimmune disease; infectious disease; graft rejection; type I diabetes;
XX KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
XX KM arteriosclerosis; inflammatory bowel disease; thyroiditis.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200248312-A2.
XX
XX 20-JUN-2002.
XX
XX 11-DEC-2001; 2001WO-1101144.
XX
XX 11-DEC-2000; 2000IL-0140233.
XX
XX (PEPT-) PEPTOR LTD.
XX
XX Elias D, Avron A, Senderowitz H;
XX WPI; 2002-557613/59.
XX
XX New backbone cyclised peptide analog of heat shock protein useful in
XX PT the treatment of e.g. autoimmune disease -
XX PS Claim 5; Page 42; 50pp; English.
XX
XX The invention relates to backbone cyclised peptide analogues or
XX CC antagonists of heat shock protein (hsp). The analogues and antagonists
XX CC are useful in the treatment of chronic inflammatory disease, autoimmune
XX CC disease, infectious disease and graft rejection, and for diagnosing
XX CC autoimmune and inflammatory disease including juvenile rheumatoid
XX CC arthritis, type I diabetes, multiple sclerosis, systemic lupus
XX CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
XX CC arteriosclerosis. This sequence represents a backbone cyclised peptide
XX CC analogue of a heat shock protein.
XX SQ Sequence 16 AA;

Query Match 100.0%; Score 87; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 VVLEKKWGAPITNDG 16
DB 1 VVLEKKWGAPITNDG 16

RESULT 3
AAU93328
ID AAU93328 standard; peptide; 22 AA.
AC AAU93328;
XX
XX 04-SEP-2000 (first entry)
XX
XX Amino acid sequence of an epitope of heat shock protein 60.
XX
XX Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
XX KM inflammatory disorder; arthritis.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200027870-A1.
XX
XX 18-MAY-2000.
XX
XX 04-NOV-1999; 99WO-1100595.
XX
XX 05-NOV-1998; 98US-0107213.
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX Neparstek Y, Ulmansky R, Kasht Y;
XX WPI; 2000-376486/32.
XX
XX Peptide having a defined sequence is used in vaccines for conferring
XX PT immunity against autoimmune disease or inflammatory disorders,
XX PT especially arthritis -
XX PS Claim 1; Page 7; 58pp; English.
XX
XX The present sequence represents an epitope of the heat shock protein
XX CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
XX CC nucleic acid encoding it, are useful in vaccines for conferring
XX CC immunity against autoimmune disease or inflammatory disorders,
XX CC especially arthritis. The peptide may also be used to raise
XX CC antibodies, which are then used for passive immunisation.
XX
XX Sequence 22 AA;
XX SQ

Query Match 100.0%; Score 87; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKWGAPITNDG 16
DB 7 VVLEKKWGAPITNDG 22

RESULT 4
AAU60145
ID AAU60145 standard; Protein; 215 AA.
AC AAU60145;
XX
XX 25-AUG-1998 (first entry)
XX
XX M. vaccae antigen GV-27A sequence.
XX
XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
XX KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
XX KM Mycobacteria infection; vaccine; cancer.
XX

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:09:39 ; Search time 21.9259 Seconds
(without alignments)
145.229 Million cell updates/sec

Title: US-09-847-637B-3
Sequence: 1 VLEKKWGAPITNDG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	US-09-847-637B-3	Sequence 3, Appl1
2	87	100.0	22	US-09-847-637B-1	Sequence 1, Appl1
3	87	100.0	215	US-09-880-505-117	Sequence 117, Appl
4	87	100.0	215	US-10-205-979-41	Sequence 41, Appl
5	87	100.0	215	US-10-051-643-117	Sequence 117, Appl
6	87	100.0	295	US-10-267-311-13	Sequence 33, Appl
7	87	100.0	523	US-09-880-505-114	Sequence 114, Appl
8	87	100.0	523	US-10-051-643-114	Sequence 114, Appl
9	87	100.0	540	US-09-847-637B-6	Sequence 6, Appl1
10	87	100.0	540	US-09-712-363-169	Sequence 169, Appl
11	87	100.0	540	US-10-267-311-4	Sequence 4, Appl1
12	87	100.0	540	US-10-046-649-3	Sequence 3, Appl1
13	87	100.0	540	US-10-046-649-4	Sequence 4, Appl1
14	87	100.0	541	US-09-880-505-160	Sequence 160, Appl
15	87	100.0	541	US-10-205-979-40	Sequence 40, Appl

16	87	100.0	541	US-10-051-643-160	Sequence 160, Appl
17	87	100.0	541	US-10-156-761-11465	Sequence 11465, A
18	87	100.0	576	US-10-369-493-8322	Sequence 8322, Ap
19	87	100.0	639	US-10-267-311-17	Sequence 17, Appl
20	87	100.0	648	US-10-267-311-29	Sequence 29, Appl
21	87	100.0	690	US-10-068-059-10	Sequence 10, Appl
22	87	100.0	709	US-10-068-059-8	Sequence 8, Appl1
23	87	100.0	724	US-10-068-059-12	Sequence 12, Appl
24	87	100.0	746	US-10-068-059-6	Sequence 6, Appl1
25	87	100.0	948	US-10-267-311-21	Sequence 21, Appl
26	81	93.1	548	US-09-738-626-6486	Sequence 6486, Ap
27	77	88.5	538	US-10-369-493-2950	Sequence 2950, Ap
28	72	82.8	542	US-10-156-761-12526	Sequence 12526, A
29	68	78.2	544	US-10-369-493-17132	Sequence 17132, A
30	68	78.2	544	US-10-369-493-23094	Sequence 23094, A
31	66	75.9	521	US-10-369-493-9597	Sequence 9597, Ap
32	66	75.9	540	US-10-369-493-15838	Sequence 15838, A
33	66	75.9	544	US-10-369-493-15468	Sequence 15468, A
34	66	75.9	544	US-10-369-493-16217	Sequence 16217, A
35	66	75.9	544	US-10-369-493-20276	Sequence 20276, A
36	66	75.9	548	US-10-369-493-513	Sequence 513, App
37	65	74.7	544	US-10-369-493-20873	Sequence 20873, A
38	65	74.7	545	US-10-228-167A-2	Sequence 2, Appl1
39	65	74.7	545	US-10-369-493-19756	Sequence 19756, A
40	64	73.6	547	US-10-369-493-10014	Sequence 10014, A
41	63	72.4	547	US-10-046-649-2	Sequence 2, Appl1
42	63	72.4	548	US-09-415-849-1	Sequence 1, Appl1
43	63	72.4	548	US-09-276-455-10	Sequence 10, Appl
44	63	72.4	551	US-10-369-493-20184	Sequence 20184, A
45	63	72.4	641	US-10-267-311-51	Sequence 51, Appl

ALIGNMENTS

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RESULT 1
US-09-847-637B-3
; Sequence 3, Application US/09847637B
; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Umanetsky, Rina
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USBS THEREOF
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-3
Query Match      100.0%; Score 87; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 VLEKKWGAPITNDG 16
Db      1 VLEKKWGAPITNDG 16
RESULT 2
US-09-847-637B-1
; Sequence 1, Application US/09847637B

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; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yakov
; APPLICANT: Umanetsky, Rina
; APPLICANT: Kash, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847, 637B
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-09-847-637B-1

Query Match      100.0%; Score 87; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLEKKKGAPTTNDG 16
DB      7 VLEKKKGAPTTNDG 22

RESULT 3
; US-09-880-505-117
; Sequence 117, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Rose
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880, 505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-09-880-505-117

Query Match      100.0%; Score 87; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLEKKKGAPTTNDG 16
DB      37 VLEKKKGAPTTNDG 52

RESULT 4
; US-10-205-979-41
; Sequence 41, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.

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; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205, 979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 215
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; ORGANISM: Mycobacterium vaccae
; US-10-205-979-41

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DB      37 VLEKKKGAPTTNDG 52

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; Sequence 117, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051, 643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 117
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; US-10-051-643-117

Query Match      100.0%; Score 87; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLEKKKGAPTTNDG 16
DB      37 VLEKKKGAPTTNDG 52

RESULT 6
; US-10-267-311-33
; Sequence 33, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267, 311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:06:09 ; Search time 11.2593 Seconds
(without alignments)
60.126 Million cell updates/sec

Title: US-09-847-637B-3

Sequence: 1 VVLEKKWGAPTITNDG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	215	2 US-08-997-080-117	Sequence 117, App
2	87	100.0	215	2 US-08-997-362-117	Sequence 117, App
3	87	100.0	215	3 US-09-095-855-117	Sequence 117, App
4	87	100.0	215	4 US-09-324-542-117	Sequence 117, App
5	87	100.0	215	4 US-09-205-426-117	Sequence 117, App
6	87	100.0	295	4 US-09-613-303-33	Sequence 33, App
7	87	100.0	523	2 US-08-997-080-114	Sequence 114, App
8	87	100.0	523	2 US-08-997-362-114	Sequence 114, App
9	87	100.0	523	3 US-09-095-855-114	Sequence 114, App
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11	87	100.0	523	4 US-09-205-426-114	Sequence 114, App
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20	87	100.0	540	5 PCT-US94-06362-3	Sequence 3, App
21	87	100.0	540	5 PCT-US94-06362-4	Sequence 4, App
22	87	100.0	541	2 US-08-467-822-34	Sequence 34, App
23	87	100.0	541	2 US-08-447-154-19	Sequence 19, App
24	87	100.0	541	2 US-08-997-080-160	Sequence 160, App
25	87	100.0	541	2 US-08-997-362-160	Sequence 160, App
26	87	100.0	541	3 US-09-095-855-160	Sequence 160, App
27	87	100.0	541	3 US-08-432-697-34	Sequence 34, App

28	87	100.0	541	3 US-08-466-248-34	Sequence 34, App
29	87	100.0	541	4 US-09-324-542-160	Sequence 160, App
30	87	100.0	541	4 US-09-205-426-160	Sequence 160, App
31	87	100.0	639	4 US-09-613-303-17	Sequence 29, App
32	87	100.0	648	4 US-09-613-303-29	Sequence 21, App
33	87	100.0	948	4 US-08-467-822-31	Sequence 31, App
34	66	75.9	548	2 US-08-432-697-31	Sequence 31, App
35	66	75.9	548	3 US-08-466-248-31	Sequence 31, App
36	66	75.9	548	3 US-08-466-248-31	Sequence 31, App
37	64	73.6	349	4 US-09-107-532A-6684	Sequence 6684, App
38	63	72.4	547	4 US-08-461-722-2	Sequence 2, App
39	63	72.4	547	4 US-08-336-251-2	Sequence 2, App
40	63	72.4	547	4 US-09-468-041-2	Sequence 2, App
41	63	72.4	547	5 PCT-US94-06362-2	Sequence 2, App
42	63	72.4	548	2 US-08-467-822-32	Sequence 32, App
43	63	72.4	548	3 US-09-472-971-3	Sequence 3, App
44	63	72.4	548	3 US-08-432-697-32	Sequence 32, App
45	63	72.4	548	3 US-08-466-248-32	Sequence 32, App

ALIGNMENTS

RESULT 1
US-08-997-080-117
Sequence 117, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-117
Query Match 100.0%; Score 87; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVLEKKWGAPTITNDG 16

Db 37 VLEKKMGAPTITNDG 52

RESULT 2
US-08-997-362-117

; Sequence 117, Application US/08997362

; Patent No. 5985287

; GENERAL INFORMATION:

; APPLICANT: Tan, Paul

; APPLICANT: Hiayama, Jun

; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot

; APPLICANT: Scott, Linda

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

; TITLES OF INVENTIONS: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

; NUMBER OF SEQUENCES: 194

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/997,362

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

; FILING DATE: June 12, 1997

; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

; FILING DATE: August 29, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1002c2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-269-0565

; TELEFAX: 206-269-0563

; TELEX:

; INFORMATION FOR SEQ ID NO: 117:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 215 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-997-362-117

Query Match 100.0%; Score 87; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTITNDG 16

Db 37 VLEKKMGAPTITNDG 52

RESULT 3
US-09-095-855-117

; Sequence 117, Application US/09095855

; Patent No. 6160093

; GENERAL INFORMATION:

; APPLICANT: Tan, Paul

; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLES OF INVENTIONS: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 29-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

; US-09-095-855-117

Query Match 100.0%; Score 87; DB 3; Length 215;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTITNDG 16

Db 37 VLEKKMGAPTITNDG 52

RESULT 4
US-09-324-542-117

; Sequence 117, Application US/09324542

; Patent No. 6328978

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L.Y.

; APPLICANT: Prestidge, Ross

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; TITLES OF INVENTIONS: of Immunologically-Mediated Skin Disorders

; FILE REFERENCE: 11000.1007c1

; CURRENT APPLICATION NUMBER: US/09/324,542

; CURRENT FILING DATE: 1999-06-02

; EARLIER APPLICATION NUMBER: US 08/997,080

; EARLIER FILING DATE: 1997-12-23

; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 117

; LENGTH: 215

; TYPE: PRT

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:21:30 ; Search time 21 Seconds
(without alignments)
100.748 Million cell updates/sec

Title: US-09-847-637B-1
Perfect score: 122
Sequence: 1 GPKGRVVLAKKMGAPITNDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 4264

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 76:*
2: PIR1:*
3: PIR2:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	30	24.6	18	1	MTDFBC
2	29	23.8	17	2	A37823
3	28	23.0	21	2	S03986
4	28	23.0	22	2	A45913
5	27	22.1	18	1	MTHOB
6	27	22.1	21	2	A42762
7	27	22.1	21	2	S62893
8	27	22.1	22	2	A12846
9	26	21.3	14	2	I54945
10	26	21.3	15	2	PI651
11	26	21.3	16	2	E58501
12	26	21.3	17	2	B53113
13	26	21.3	19	2	PX0062
14	25	20.5	13	1	MTCMAD
15	25	20.5	13	1	MTMOAD
16	25	20.5	17	2	S03531
17	25	20.5	18	1	DRUPFD
18	25	20.5	18	2	A29558
19	25	20.5	20	2	S46488
20	25	20.5	21	2	S33287
21	25	20.5	21	2	PC1310
22	24.5	20.1	17	2	PH1557
23	24	19.7	15	2	UN0730
24	24	19.7	20	2	PQ0071
25	24	19.7	21	2	I54268
26	23.5	19.3	20	2	S29635
27	23	18.9	11	2	A34243
28	23	18.9	15	2	PH0760
29	23	18.9	22	2	UC0009

30	23	18.9	22	2	A28563	hemoglobin chain I
31	22.5	18.4	20	2	P42762	proteasome endopep
32	22.5	18.4	20	2	PH1380	alpha-amylase (EC
33	22	18.0	8	2	A31570	angiotensin-conver
34	22	18.0	13	2	G83988	hypothetical prote
35	22	18.0	17	2	S77834	DNA-directed RNA p
36	22	18.0	18	2	G84114	hypothetical prote
37	22	18.0	20	2	S29636	hypothetical prote
38	22	18.0	20	2	S10876	jacalin beca-I cha
39	22	18.0	21	2	S71602	hypothetical prote
40	22	18.0	22	2	PQ0070	recombinational prot
41	21.5	17.6	17	2	S24570	T-cell receptor be
42	21.5	17.6	20	2	S03987	Ig heavy chain J r
43	21	17.2	11	2	S09074	agglutinin beta-2
44	21	17.2	11	2	YHRT	cytochrome P450-4b
45	21	17.2	11	2	YHRT	morphogenetic neur

ALIGNMENTS

RESULT 1
MTDFBC
melanotropin beta - smaller spotted catshark
C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C/Accession: A01470
R/Love, R.M.; Pickering, B.T.
Gen. Comp. Endocrinol. 24, 398-404, 1974
A/Title: A beta-MSH in the pituitary gland of the spotted dogfish (Scyliorhinus canicula)
A/Reference number: A01470; MUID:75113445; PMID:4452470
A/Accession: A01470
A/Molecule type: protein
A/Residues: 1-18 <LOV>
C/Superfamily: corticotropin-lipotropin
C/Keywords: hormone

Query Match 24.6%; Score 30; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KWGAP 16
DB 11 RWGAP 15

RESULT 2
A37823
dihydroliipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-May-2000
C/Accession: A37823
R/Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.
J. Biol. Chem. 265, 14512-14517, 1990
A/Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon selec
A/Reference number: A37823; MUID:90354445; PMID:2167319
A/Accession: A37823
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-17 <RAH>
C/Keywords: acyltransferase; coenzyme A

Query Match 23.8%; Score 29; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGR 5
DB 1 GPKGR 5

RESULT 3
S03986

agglutinin beta-1 chain - Oseage orange
 C/Species: Maciura pomifera (Oseage orange)
 C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 01-Aug-1997
 C/Accession: S03986; S03988
 R/Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.
 Arch. Biochem. Biophys. 270, 596-603, 1989
 A/Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia and M
 A/Reference number: S03983; MUID:89206218; PMID:2705782
 A/Accession: S03986
 A/Molecule type: protein
 A/Residues: 1-21 <Y0U>
 A/Note: beta-1 form
 A/Accession: S03988
 A/Molecule type: protein
 A/Residues: 2-21 <Y02>
 A/Note: beta-3 form

Query Match 23.0%; Score 28; DB 2; Length 21;
 Best Local Similarity 33.3%; Pred. No. 9.2e+02;
 Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

QY 1 GPKGRN-VVLEKKGAPITN 20
 |||:::|||||:
 Db 2 GPKGKSOSITVGPWG-DVITN 21

RESULT 4
 A45913
 plantaricin A - Lactobacillus plantarum
 C/Species: Lactobacillus plantarum
 C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 12-Sep-1997
 C/Accession: A45913
 R/Nissen-Meyer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.
 submitted to the Protein Sequence Database, April 1993
 A/Reference number: A45913
 A/Accession: A45913
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-22 <NIS>
 C/Keywords: antibiotic, bacteriocin

Query Match 23.0%; Score 28; DB 2; Length 22;
 Best Local Similarity 83.3%; Pred. No. 9.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 LEXKKG 14
 |||||
 Db 17 LFRKKG 22

RESULT 5
 MTHOB
 melanotropin beta - horse
 C/Species: Equus caballus (domestic horse)
 C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
 C/Accession: A01467
 R/Dixon, J.S.; Li, C.H.
 Gen. Comp. Endocrinol. 1, 161-169, 1961
 A/Title: The isolation and structure of beta-melanocyte-stimulating hormone from horse p
 A/Reference number: A01467
 A/Accession: A01467
 A/Molecule type: protein
 A/Residues: 1-18 <DIX>
 C/Superfamily: corticotropin-11pocropin
 C/Keywords: hormone

Query Match 22.1%; Score 27; DB 1; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 KMGAP 16
 |||:
 Db 11 RMGSP 15

RESULT 6
 A42762
 proteasome endopeptidase complex (BC 3.4.25.1) subunit 13 - Bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003
 C/Accession: A42762
 R/Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
 Biochemistry 31, 7347-7355, 1992
 A/Title: Identification and localization of a cysteinyl residue critical for the tryp:
 A/Reference number: A42762; MUID:92378961; PMID:1510924
 A/Accession: A42762
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-21 <DIC>
 A/Note: sequence extracted from NCBI backbone (NCBIP:112172)
 C/Superfamily: multicatalytic endopeptidase complex chain C9
 C/Keywords: hydrolase

Query Match 22.1%; Score 27; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 14 GAPITND 21
 |||:
 Db 8 GCPWVTD 15

RESULT 7
 S62893
 cold-inducible protein, 70K - rainbow trout (fragment)
 C/Species: Oncorhynchus mykiss (rainbow trout)
 C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
 C/Accession: S62893
 R/Yamashita, M.; Ojima, N.; Sakamoto, T.
 FEBS Lett. 382, 261-264, 1996
 A/Title: Induction of proteins in response to cold acclimation of rainbow trout cells.
 A/Reference number: S62893; MUID:96184500; PMID:8605981
 A/Accession: S62893
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-21 <YAM>

Query Match 22.1%; Score 27; DB 2; Length 21;
 Best Local Similarity 46.7%; Pred. No. 1.3e+03;
 Matches 7; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 GPKGRNVVLEKKGCA 15
 |||:
 Db 6 GPKGTGKML--IWCA 18

RESULT 8
 A12846
 hypothetical protein Atu2202 [imported] - Agrobacterium tumefaciens (strain C58, Dupont
 C/Species: Agrobacterium tumefaciens
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C/Accession: A12846
 R/Wood, D.W.; Sebda, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCle,
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
 ster, E.W.
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: A12846
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-22 <KUR>
 A/Cross-references: GB:AB006688; PIDN:AAI43191.1; PID:917740671; GSPDB:GN00186
 A/Experimental source: strain C58 (Dupont)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:12:10 ; Search time 11 Seconds
(without alignments)
94.053 Million cell updates/sec

Title: US-09-847-637B-1

Sequence: 1 GPKGRNVVLEKKMGAPITINDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 1361

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	25.4	19	1	CH10_CLOPA
2	30	24.6	18	1	MLB_SCYCA
3	28	23.0	20	1	LEC3_MACRO
4	28	23.0	21	1	LEC1_MACRO
5	27	22.1	17	1	PLA2_BARBA
6	27	22.1	18	1	MLB_HORSE
7	25	20.5	13	1	MLA_ANOCA
8	25	20.5	13	1	MLA_CAMDR
9	25	20.5	15	1	UNO1_PINPS
10	25	20.5	18	1	DRPH_UCAPU
11	24	19.7	21	1	LEC2_ARTIN
12	23	18.9	11	1	ASL2_BACSE
13	23	18.9	20	1	LEC1_ARTIN
14	23	18.9	21	1	UAP2_RANTA
15	23	18.9	22	1	HGL2_FASHE
16	23	18.9	22	1	PA2_DABRU
17	22	18.0	8	1	ACI_THUL
18	22	18.0	10	1	UHA3_HUMAN
19	22	18.0	20	1	LEC3_ARTIN
20	22	18.0	22	1	BS23_SERPL
21	22	18.0	22	1	LEC2_MACRO
22	21.5	17.6	20	1	MORN_HUMAN
23	21	17.2	20	1	VAR9_BORPE
24	21	17.2	20	1	SC1B_BPTS
25	21	17.2	21	1	LIGA_TRAVE
26	20	16.4	13	1	UNO2_PINPS
27	20	16.4	13	1	MCRX_METTM
28	20	16.4	16	1	MLB_SQUAC
29	20	16.4	18	1	AGI_EUPCH
30	20	16.4	19	1	AB27_CYPCH
31	20	16.4	19	1	PGK_BACCE
32	20	16.4	20	1	TPX_CLOPA
33	20	16.4	20	1	TPX_CLOPA

34	20	16.4	22	1	DEP1_SPIOL
35	19	15.6	9	1	TRH1_LOCMT
36	19	15.6	10	1	BP22_BOTUA
37	19	15.6	11	1	CEP1_ACHFU
38	19	15.6	12	1	UP01_CABEL
39	19	15.6	13	1	IDHP_RAT
40	19	15.6	13	1	LIGB_TRAVE
41	19	15.6	14	1	SAP2_ARBPV
42	19	15.6	15	1	UC06_MAIZR
43	19	15.6	16	1	MMPX_SOLTU
44	19	15.6	18	1	AGI_BUPMA
45	19	15.6	20	1	PGK_CLOPA

ALIGNMENTS

```

RESULT 1
CH10_CLOPA          STANDARD; PRT; 19 AA.
ID_MLB_SCYCA
AC_P01206;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 10 kDa chaperonin (Protein Cpn10) (groES protein) (CP 31) (Fragment).
GN GROS OR GROES.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RL sequence analysis of proteins from Clostridium pasteurianum W5."
CC Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses
CC the ATPase activity of the latter.
CC -1- SUBUNIT: Heptamer of 7 subunits arranged in a ring (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GROS CHAPERONIN FAMILY.
DR HAMAP; MF_00580; -; 1.
DR InterPro; IPR001476; Chaperin_Cpn10.
DR Pfam; PF00166; Cpn10; 1.
DR PROSITE; PS00661; CHAPERONINS_CPN10; PARTIAL.
KW Chaperone.
FT NON_TER
SQ SEQUENCE 19 AA; 2026 MW; 7D6B9BD414E60A60 CRC64;
Query Match 25.4%; Score 31; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PKGRNVVLEK 11
Db 5 PLGDNVVLEK 14
RESULT 2
MLB_SCYCA          STANDARD; PRT; 18 AA.
ID_MLB_SCYCA
AC_P01206;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanocortropin beta (Beta-MSH).
OS Melanocortropin canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryotes; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.

```

OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75113445; PubMed=4452470;
 RA Love R.M., Pickering B.T.;
 RT "A beta-MSH in the pituitary gland of the spotted dogfish (Scyliorhinus canicula): isolation and structure.";
 RL Gen. Comp. Endocrinol. 24:398-404(1974).
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
 DR PIR; A01470; MTDPRC.
 KW Hormone.
 SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;
 QY
 DB 12 KMGAP 16
 11 RMGAP 15
 Query Match 24.6%; Score 30; DB 1; Length 18;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 LEC3_MACPO STANDARD; PRT; 20 AA.
 ID LEC3_MACPO
 AC P18677;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE Agglutinin beta-3 chain (MPA).
 OS MacLura pomifera (Obage orange).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Moraceae; MacLura.
 OX NCBI_TaxID=3496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=89206218; PubMed=2705782;
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
 RT "Homology of the D-galactose-specific lectins from Artocarpus integrifolia and MacLura pomifera and the role of an unusual small RT polypeptide subunit.";
 RL Arch. Biochem. Biophys. 270:596-603(1989).
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN STRUCTURE GAL-BETA1-3-GALNAc.
 CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
 DR HSSP; P18676; IJOT.
 KW Lectin.
 SQ SEQUENCE 20 AA; 2082 MW; AA38811BBD6370E0 CRC64;
 QY
 DB 1 GPKGRN-VLEKKWGAPITN 20
 1 GPNKGSOSIIVGPMG-DRVTN 20
 Query Match 23.0%; Score 28; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 5.3e+02;
 Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

RESULT 4
 LEC1_MACPO STANDARD; PRT; 21 AA.
 ID LEC1_MACPO
 AC P18675;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE Agglutinin beta-1 chain (MPA).
 OS MacLura pomifera (Obage orange).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Moraceae; MacLura.

OX NCBI_TaxID=3496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=89206218; PubMed=2705782;
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
 RT "Homology of the D-galactose-specific lectins from Artocarpus integrifolia and MacLura pomifera and the role of an unusual small RT polypeptide subunit.";
 RL Arch. Biochem. Biophys. 270:596-603(1989).
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN STRUCTURE GAL-BETA1-3-GALNAc.
 CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
 DR PIR; S03986; S03986.
 DR HSSP; P18676; IJOT.
 KW Lectin.
 SQ SEQUENCE 21 AA; 2196 MW; AA38811BCLHFD0E0 CRC64;
 QY
 DB 1 GPKGRN-VLEKKWGAPITN 20
 2 GPNKGSOSIIVGPMG-DRVTN 21
 Query Match 23.0%; Score 28; DB 1; Length 21;
 Best Local Similarity 33.3%; Pred. No. 5.5e+02;
 Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

RESULT 5
 FLA2_BARBA STANDARD; PRT; 17 AA.
 ID FLA2_BARBA
 AC P35634;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Flagellin: (Fragment).
 OS Bartonella bacilliformis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bartonellaceae; Bartonella.
 OX NCBI_TaxID=774;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=KC584;
 RX MEDLINE=94041612; PubMed=8225570;
 RA Scherer D.C., Debucun-Cormore I., Minnick M.F.;
 RT "Characterization of Bartonella bacilliformis flagella and effect of anti-flagellin antibodies on invasion of human erythrocytes";
 RL Infect. Immun. 61:4962-4971(1993).
 CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMENTS OF BACTERIAL FLAGELLA. FLAGELLA ARE AN IMPORTANT COMPONENT IN THE INVASIVENESS OF B. BACILLIFORMIS.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
 DR NON_TER
 KW Flagella.
 SQ SEQUENCE 17 AA; 1746 MW; BA24BE61778CDB8 CRC64;
 QY
 DB 14 GAPITND 21
 1 GAAILTND 8
 Query Match 22.1%; Score 27; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 6.4e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 6
 MLB_HORSE STANDARD; PRT; 18 AA.
 ID MLB_HORSE
 AC P01202;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin beta (Beta-MSH).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:20:40 ; Search time 33 Seconds
(without alignments)
172.035 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVLEKKGAPITNDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 8134

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_ivirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	28.7	18	6	Q9TRD8
2	27.5	22.5	16	4	Q9UCR9
3	27	22.1	17	4	Q9UPK4
4	27	22.1	21	13	Q9PRQ1
5	27	22.1	22	2	Q9AH71
6	27	22.1	22	13	Q9PRN2
7	27	22.1	22	16	Q9UCR5
8	26	21.3	14	2	Q47599
9	26	21.3	17	2	Q9R512
10	26	21.3	18	4	Q9NFB4
11	26	21.3	18	15	Q73920
12	26	21.3	18	15	Q73921
13	25	20.5	10	11	Q70580
14	25	20.5	16	2	Q45530
15	25	20.5	17	4	Q9UC91
16	25	20.5	19	13	Q9PRN4

17	25	20.5	20	13	Q9PRN3	Q9PRN3 petromyzon
18	25	20.5	20	15	Q73918	Q73918 human immun
19	25	20.5	20	15	Q73917	Q73917 human immun
20	25	20.5	21	2	Q9AJG0	Q9AJG0 vibrio pela
21	25	20.5	21	5	Q9TMO5	Q9TMO5 tachyleus
22	25	20.5	22	11	Q9OMB6	Q9OMB6 mus sp. sgp
23	25	20.5	22	13	Q90ZY4	Q90ZY4 rallus lima
24	25	20.5	22	13	Q90ZY2	Q90ZY2 sarothrua
25	25	20.5	22	13	Q90ZY3	Q90ZY3 rallus long
26	25	20.5	22	13	Q910C6	Q910C6 gallinula c
27	24	19.7	10	4	Q9UNP2	Q9UNP2 homo sapien
28	24	19.7	15	2	Q9R4P5	Q9R4P5 brewidmon
29	24	19.7	17	6	Q93395	Q93395 canis famli
30	24	19.7	18	6	Q9N1D5	Q9N1D5 canis famli
31	24	19.7	18	15	Q73487	Q73487 human immun
32	24	19.7	20	1	Q9UMM8	Q9UMM8 halobacteri
33	24	19.7	20	10	P83423	P83423 morus nigra
34	24	19.7	20	10	P83426	P83426 morus nigra
35	24	19.7	21	4	Q15965	Q15965 homo sapien
36	24	19.7	22	1	Q9UW19	Q9UW19 methanospir
37	23.5	19.3	20	10	Q9S8R1	Q9S8R1 artocarpus
38	23	18.9	11	15	Q83410	Q83410 mouse mamma
39	23	18.9	13	15	Q85645	Q85645 mouse mamma
40	23	18.9	16	2	Q10748	Q10748 clostridium
41	23	18.9	16	4	Q9UC18	Q9UC18 homo sapien
42	23	18.9	16	8	Q9T2V8	Q9T2V8 homo sapien
43	23	18.9	16	10	Q9S8D6	Q9S8D6 triticum ae
44	23	18.9	17	4	Q9UCF0	Q9UCF0 homo sapien
45	23	18.9	17	8	Q03888	Q03888 chlorogonlu

ALIGNMENTS

RESULT 1

Q9TRD8 PRELIMINARY; PRT; 18 AA.

AC Q9TRD8; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE Chapteronin (Fragment).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NC NCI_TaxID=9986;

RN [1]

RP SEQUENCE.

RX MEDLINE=94089752; PubMed=7903455;

RA Rommelaere H., Van Troys M., Gao Y., Melki R., Cowan N.J.,

RA Vandekekerckhove J., Ampe C.;

RT "Eukaryotic cytosolic chaperonin contains c-complex polypeptide 1 and

RT seven related subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:11975-11979(1993).

SO SEQUENCE 18 AA; 1884 MW; B608F6EB5A8A246 CRC64;

Query Match 28.7%; Score 35; DB 6; Length 18;

Best local similarity 46.7%; Pred. No. 1.5e+02;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 VLEKKGAPITNDG 22

DB 1 MMTDKDGVTVTNDG 15

RESULT 2

Q9UCR9 PRELIMINARY; PRT; 16 AA.

AC Q9UCR9; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)

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DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099171; PubMed=1463770;
RA Baba S., Takahashi T., Kasama T., Shiraawa H.;
RT "Identification of two novel amyloid A protein subsets coexisting in
RT an individual patient of AA-amyloidosis."
RL Biochim. Biophys. Acta 1180:195-200(1992).
CC -1- FUNCTION: MAJOR ACTIN PHASE REACTANT. APOLOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR InterPro: IPR000096; Serum_amyloid_A.
KW Acute phase; HDL.
SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8CC1 CRC64;

Query Match 22.1%; Score 27.5; DB 4; Length 16;
Best Local Similarity 35.0%; Pred. No. 2e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 7; Gaps 1;

OY 1 GPKGRNVLEKKGAPTTN 20
DB 2 GPGG-----AMAEVTSN 14

RESULT 3
O9UPK4 PRELIMINARY; PRT; 17 AA.
AC O9UPK4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE UCRY_HUMAN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerlin J.R., McCreedy P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez W., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Altik C., Andreise T., Frankheim M., Antico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 3.5 kb contig in human 19p13.3 containing a
RT serine protease gene cluster."
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; ACC05321; AAC27374.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 2166 MW; B73A34E7EDB2B5D CRC64;

Query Match 22.1%; Score 27; DB 4; Length 17;
Best Local Similarity 46.2%; Pred. No. 2.6e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 GPKGRNVLEKKG 13
DB 7 GPRRYELV--KNW 17

RESULT 4
O9PRO1 PRELIMINARY; PRT; 21 AA.
AC O9PRO1;

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DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE 70 kDa cold acclimation-related protein (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proleptoceratopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=96184500; PubMed=8605981;
RA Yamashita M., Ojima N., Sakamoto T.;
RT "Induction of proteins in response to cold acclimation of rainbow
RT trout cells."
RL FEBS Lett. 382:261-264(1996).
SQ SEQUENCE 21 AA; 2129 MW; FF68D74564917510 CRC64;

Query Match 22.1%; Score 27; DB 13; Length 21;
Best Local Similarity 46.7%; Pred. No. 3.2e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

OY 1 GPKGRNVLEKKG 15
DB 6 GPGTGKML--TWGA 18

RESULT 5
O9AH71 PRELIMINARY; PRT; 22 AA.
AC O9AH71;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hmbr (Fragment).
GN Hmbr.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=44/76;
RX MEDLINE=21116988; PubMed=11179344;
RA Kahler C.M., Blum E., Miller Y.K., Ryan D., Popovic T., Stephens D.S.;
RT "xrl, an exchangeable genetic island in Neisseria meningitidis."
RL Infect. Immun. 69:1687-1696(2001).
DR EMBL; AF319527; AAK08019.1; -.
FT NON TER 1
SQ SEQUENCE 22 AA; 2584 MW; F1BBBC6F2F3C2C49 CRC64;

Query Match 22.1%; Score 27; DB 2; Length 22;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 GRNVLEKKG 13
DB 11 GRNVAVSLHW 20

RESULT 6
O9PRN2 PRELIMINARY; PRT; 22 AA.
AC O9PRN2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Corticotropin, ACTH.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]

```


1	122	100.0	22	21	AA93338	Amino acid sequenc
2	90	73.8	16	21	AA93339	Amino acid sequenc
3	90	73.8	16	23	AA93964	Amino acid sequenc
4	87	71.3	16	18	AA43458	Mycobacteri
5	87	71.3	16	21	AA93330	Mycobacteri
6	87	71.3	16	23	AA93965	Amino acid sequenc
7	83	68.0	15	17	AA93479	Mycobacterium tube
8	83	68.0	15	18	AA43457	Mycobacteri
9	82	67.2	16	17	AA93476	Mycobacteri

10	70	57.4	15	18	AAW43459	Mycobacteria sp. h
11	65	53.3	15	17	AAW47811	Peptide from libra
12	59	48.4	20	21	AAV93311	Amino acid sequenc
13	59	48.4	20	23	AAU93986	Mycobacterium tuberc
14	57	46.7	16	17	AAW47778	Peptide from libra
15	47	46.7	16	18	AAW43456	Mycobacteria sp. h
16	47	38.5	11	22	AAW88272	Hsp-65 peptide epi
17	43	35.2	10	22	AAW88269	Hsp-65 peptide epi
18	42	34.4	20	10	AAW91037	Amino acids 1021-1
19	42	34.4	20	19	AAW68009	Tetanus toxin T-ce
20	39	32.0	9	22	AAW88279	Hsp-65 peptide epi
21	39	32.0	15	23	AAW26843	Anabaena variabilis
22	39	32.0	16	18	AAW43460	Mycobacteria sp. h
23	39	32.0	17	17	AAW94777	Peptide from libra
24	39	32.0	17	18	AAW43455	Mycobacteria sp. h
25	36	29.5	20	22	ABW54567	Human liver peptid
26	36	29.5	20	22	ABW39610	Peptide #716 enco
27	36	29.5	20	22	AAW60314	Human brain express
28	36	29.5	20	22	AAW72948	Human bone marrow
29	36	29.5	20	23	AAW33173	Peptide #721 enco
30	36	29.5	20	23	ABW42875	Human peptide enco
31	35	28.7	16	16	AAW87908	Bovine lactoferrin
32	35	28.7	16	17	AAW10516	Lactoferrin derive
33	35	28.7	18	15	AAW69334	Bovine lactoferrin
34	35	28.7	18	17	AAW10515	Lactoferrin derive
35	35	28.7	19	23	AAU90668	Insulin/insulin-ii
36	35	28.7	20	13	AAW21808	Anti microbial pep
37	35	28.7	20	13	AAW21809	Anti microbial pep
38	35	28.7	20	14	AAW44840	Lactoferrin-relate
39	35	28.7	20	15	AAW48528	Lactoferrin derive
40	35	28.7	20	15	AAW48529	Lactoferrin derive
41	35	28.7	20	15	AAW57459	Lactoferrin derive
42	35	28.7	20	15	AAW57460	Lactoferrin derive
43	35	28.7	20	16	AAW84656	Bovine lactoferrin
44	35	28.7	20	16	AAW84657	Bovine lactoferrin
45	35	28.7	20	16	AAW80261	Anti-parasitic lac

RESULT 1
AA93328

XX	AA93328 standard; peptide; 22 AA.
XX	AA93328;
AC	
DT	04-SEP-2000 (first entry)
DE	
XX	Amino acid sequence of an epitope of heat shock protein 60.
XX	
XX	Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KW	inflammatory disorder; arthritis.
XX	
OS	Mycobacterium tuberculosis.
XX	
FN	WO200027870-A1.
PD	
PD	18-MAY-2000.
XX	
PE	04-NOV-1999; 99WO-IL00595.
XX	
PR	05-NOV-1998; 98US-0107213.
XX	
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX	
FI	Naparetek Y, Ulimansky R, Kaashi Y;
XX	
DR	WPI; 2000-376486/32.
XX	
PT	Peptide having a defined sequence is used in vaccines for conferring
PT	immunity against autoimmune disease or inflammatory disorders,
PT	especially arthritis -

XX PS Claim 1; Page 7; 58pp; English.

XX CC The present sequence represents an epitope of the heat shock protein

CC 60 (hsp60) of Mycobacterium tuberculosis. The peptide, and the

CC nucleic acid encoding it, are useful in vaccines for conferring

CC immunity against autoimmune disease or inflammatory disorders,

CC especially arthritis. The peptide may also be used to raise

CC antibodies, which are then used for passive immunisation.

XX SQ Sequence 22 AA;

QY Query Match 100.0%; Score 122; DB 21; Length 22;

DB Best Local Similarity 100.0%; Pred. No. 3.9e-13;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPKGRNVVLEKKMGAPITINDG 22

1 GPKGRNVVLEKKMGAPITINDG 22

DB 1 GPKGRNVVLEKKMGAPITINDG 22

RESULT 2

AA93329 standard; peptide; 16 AA.

AA93329;

04-SEP-2000 (first entry)

Amino acid sequence of an epitope of heat shock protein 60.

Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;

inflammatory disorder; arthritis.

Myobacterium tuberculosis.

WO200027870-A1.

18-MAY-2000.

04-NOV-1999; 99WO-IL00595.

05-NOV-1998; 98US-0107213.

(HADA-) HADASIT MEDICAL RES SERVICES & DEV.

Napartek Y, Umaneky R, Kaahi Y;

WPI; 2000-376486/32.

Peptide having a defined sequence is used in vaccines for conferring

immunity against autoimmune disease or inflammatory disorders,

especially arthritis -

Claim 2; Page 7; 58pp; English.

The present sequence represents an epitope of the heat shock protein

60 (hsp60) of Mycobacterium tuberculosis. The peptide, and the

nucleic acid encoding it, are useful in vaccines for conferring

immunity against autoimmune disease or inflammatory disorders,

especially arthritis. The peptide may also be used to raise

antibodies, which are then used for passive immunisation.

SQ Sequence 16 AA;

QY Query Match 73.8%; Score 90; DB 21; Length 16;

DB Best Local Similarity 100.0%; Pred. No. 5.6e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPKGRNVVLEKKMGAP 16

1 GPKGRNVVLEKKMGAP 16

RESULT 3

AAU99964 standard; Peptide; 16 AA.

AAU99964;

07-OCT-2002 (first entry)

Myobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.

Heat shock protein; hsp; hsp60; chronic inflammatory disease;

autoimmune disease; infectious disease; graft rejection; type I diabetes;

juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;

systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.

arteriosclerosis.

Myobacterium tuberculosis.

WO200248312-A2.

20-JUN-2002.

11-DEC-2001; 2001WO-IL01144.

11-DEC-2000; 2000IL-0140233.

(PEPT-) PEPTOR LTD.

Elias D, Avron A, Senderowitz H;

WPI; 2002-557613/59.

New backbone cyclised peptide analog of heat shock protein useful in

the treatment of e.g. autoimmune disease -

Claim 5; Page 42; 50pp; English.

The invention relates to backbone cyclised peptide analogues or

antagonists of heat shock protein (hsp). The analogues and antagonists

are useful in the treatment of chronic inflammatory disease, autoimmune

disease, infectious disease and graft rejection, and for diagnosing

autoimmune and inflammatory disease including juvenile rheumatoid

arthritis, type I diabetes, multiple sclerosis, systemic lupus

erythematosus, inflammatory bowel disease, uveitis, thyroiditis and

arteriosclerosis. This sequence represents a backbone cyclised peptide

analogue of a heat shock protein.

SQ Sequence 16 AA;

QY Query Match 73.8%; Score 90; DB 23; Length 16;

DB Best Local Similarity 100.0%; Pred. No. 5.6e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPKGRNVVLEKKMGAP 16

1 GPKGRNVVLEKKMGAP 16

RESULT 4

AAW43458 standard; peptide; 16 AA.

AAW43458;

08-APR-1998 (first entry)

Myobacteria sp. hsp68 derived peptide (group 1 #8).

Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;

rheumatoid arthritis; antigen; infectious disease; prophylactic;

pristane induced arthritis; PIA.

OS Synthetic.
 OS Mycobacteria sp.
 XX
 XX WO9711966-A1.
 PN
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-GB02382.
 XX
 PR 27-SEP-1995; 95GB-0019737.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
 XX
 PI Elson CJ, Thompson JS;
 DR WPI; 1997-212851/19.
 XX
 PT Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis
 XX
 PS Disclosure; Fig 1a; 91pp; English.
 XX
 CC This peptide is one of a library (see AAM43451-W4356) which represents
 the mycobacterial heat shock protein, hsp65 and is designed to study
 a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAM43458-W43950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.
 XX
 SQ Sequence 16 AA;
 QY
 DB 6 NVVLEKKMGAPTTND 21
 1 NVVLEKKMGAPTTND 16
 Query Match 71.3%; Score 87; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 AAY93330
 ID AAY93330 standard; peptide; 16 AA.
 XX
 AC AAY93330;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of an epitope of heat shock protein 60.
 XX
 KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
 inflammatory disorder; arthritis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200027870-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 04-NOV-1999; 99WO-IL00595.
 XX
 PR 05-NOV-1998; 98US-0107213.
 XX
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 XX
 PI Naparstek Y, Ulimansky R, Kaehl Y;

XX
 DR WPI; 2000-376486/32.
 XX
 PT Peptide having a defined sequence is used in vaccines for conferring
 immunity against autoimmune disease or inflammatory disorders,
 especially arthritis -
 XX
 PS Claim 3; Page 7; 58pp; English.
 XX
 CC The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX
 SQ Sequence 16 AA;
 QY
 DB 7 VVLEKKMGAPTTNDG 22
 1 VVLEKKMGAPTTNDG 16
 Query Match 71.3%; Score 87; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 AAU99965
 ID AAU99965 standard; Peptide; 16 AA.
 XX
 AC AAU99965;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.
 XX
 KW Heat shock protein; hsp; hsp60; chronic inflammatory disease;
 KW autoimmune disease; infectious disease; graft rejection; type I diabetes;
 KW juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
 KW systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200248312-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 11-DEC-2001; 2001WO-IL01144.
 XX
 PR 11-DEC-2000; 2000IL-0140233.
 XX
 PA (PEPT-) PEPTOR LTD.
 XX
 PI Elias D, Avron A, Senderowitz H;
 XX
 DR WPI; 2002-557613/59.
 XX
 PT New backbone cyclized peptide analog of heat shock protein useful in
 the treatment of e.g. autoimmune disease -
 XX
 PS Claim 5; Page 42; 50pp; English.
 XX
 CC The invention relates to backbone cyclised peptide analogues or
 CC antagonists of heat shock protein (hsp). The analogues and antagonists
 CC are useful in the treatment of chronic inflammatory disease, autoimmune
 CC disease, infectious disease and graft rejection, and for diagnosing
 CC autoimmune and inflammatory disease including juvenile rheumatoid
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide
 CC analogue of a heat shock protein.

```

XX Sequence 16 AA;
SQ Query Match 71.3%; Score 87; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVLEKKGAPITINDG 22
DB 1 VVLEKKGAPITINDG 16

RESULT 7
AAR94779
ID AAR94779 standard; peptide; 15 AA.
AC AAR94779;
XX
XX
XX 11-NOV-1996 (first entry)
DE Peptide from library spanning whole of hsp65.
XX
XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
XX Synthetic.
XX
XX W09610039-A1.
XX
XX 04-APR-1996.
XX
XX 27-SEP-1995; 95MO-GB02295.
XX
XX 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI; 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
XX whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX prepared from the library and used to immunise mice, after 10 days the
XX mice received injections of pristane to induce arthritis and the
XX animals examined for incidence of arthritis. A preferred anti-arthritis
XX peptide was found to correspond to residues 21-31 of full length hsp65
XX (see AAR94772). Peptides concy. this sequence are used in the diagnosis,
XX treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX diseases such as rheumatoid arthritis.
XX
XX Sequence 15 AA;

Query Match 68.0%; Score 83; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKWGA 15
DB 1 GPKGRNVVLEKKWGA 15

RESULT 8
AAM43457
ID AAM43457 standard; peptide; 15 AA.
XX

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AC AAM43457;
XX
XX 08-APR-1998 (first entry)
DE Mycobacteria sp. hsp68 derived peptide (group 1 #7).
XX
XX Heat shock protein; hsp68; autoimmune disease; hsp65; vaccine;
XX rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX pristane induced arthritis; PIA.
XX
XX Synthetic.
XX
XX Mycobacteria sp.
XX
XX W09711966-A1.
XX
XX 03-APR-1997.
XX
XX 26-SEP-1996; 96MO-GB02382.
XX
XX 27-SEP-1995; 95GB-0019737.
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
XX Elson CJ, Thompson JS;
XX
XX WPI; 1997-212851/19.
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
XX for treatment of autoimmune disease esp. arthritis
XX
XX Disclosure; Fig 1a; 91pp; English.
XX
XX This peptide is one of a library (see AAM43451-W4356) which represents
XX the mycobacterial heat shock protein, hsp65 and is designed to study
XX a novel method for the treatment of autoimmune disease e.g. rheumatoid
XX arthritis. This fragment has been allocated as a group 1 peptide which
XX is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
XX hsp65 is known to be an immunodominant antigen in a number of infectious
XX diseases and is linked to pristane induced arthritis (PIA) in vitro,
XX however heat shock proteins and peptides derived from microbial sources
XX may act as self antigens and thus have limited clinical use. The human
XX hsp65 homologue, hsp58, or fragments of the hsp58 protein
XX (see AAM43451-W4350) may be useful in the development of vaccines for
XX prophylaxis or treatment of an autoimmune disease such as rheumatoid
XX arthritis.
XX
XX Sequence 15 AA;

Query Match 68.0%; Score 83; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVVLEKKWGA 15
DB 1 GPKGRNVVLEKKWGA 15

RESULT 9
AAR94780
ID AAR94780 standard; peptide; 16 AA.
AC AAR94780;
XX
XX 11-NOV-1996 (first entry)
DE Peptide from library spanning whole of hsp65.
XX
XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
XX Synthetic.
XX

```

PN MO9610039-A1.
 XX
 PD 04-APR-1996.
 XX
 PF 27-SEP-1995; 95WO-GB02295.
 XX
 PR 27-SEP-1994; 94GB-0019553.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Elson CJ, Thompson SJ;
 XX
 DR WPI; 1996-200886/20.
 XX
 PT Polypeptide derived from bacterial heat shock protein 65 - for use
 XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 XX rheumatoid arthritis.
 XX
 PS Example 1; Figure 1; 88pp; English.
 XX
 CC AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.
 XX
 SQ Sequence 16 AA;
 XX
 Query Match 67.2%; Score 82; DB 17; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.2e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 NVVLEKKMGAPTTND 21
 DB 1 NVVLEKKMGAPTTND 16
 XX
 RESULT 10
 AAW43459
 ID AAW43459 standard; peptide; 15 AA.
 XX
 AC AAW43459;
 XX
 DT 08-APR-1998 (first entry)
 XX
 DE Mycobacteria sp. hsp68 derived peptide (group 1 #9).
 XX
 KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KW pristane induced arthritis; PIA.
 XX
 OS Synthetic.
 OS Mycobacteria sp.
 XX
 PN MO9711966-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-GB02382.
 XX
 PR 27-SEP-1995; 95GB-0019737.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
 XX
 PI Elson CJ, Thompson SJ;
 XX
 DR WPI; 1997-212851/19.
 XX
 PT Polypeptide(s) derived from microbial heat shock protein - useful

PT for treatment of autoimmune disease esp. arthritis
 XX
 PS Disclosure; Fig 1a; 91pp; English.
 XX
 CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW1948-W14950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 57.4%; Score 70; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 KKGAPTTNDG 22
 DB 1 KKGAPTTNDG 12
 XX
 RESULT 11
 AAR94781
 ID AAR94781 standard; peptide; 15 AA.
 XX
 AC AAR94781;
 XX
 DT 11-NOV-1996 (first entry)
 XX
 DE Peptide from library spanning whole of hsp65.
 XX
 KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KW prophylaxis.
 XX
 OS Synthetic.
 OS
 PN MO9610039-A1.
 XX
 PD 04-APR-1996.
 XX
 PF 27-SEP-1995; 95WO-GB02295.
 XX
 PR 27-SEP-1994; 94GB-0019553.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Elson CJ, Thompson SJ;
 XX
 DR WPI; 1996-200886/20.
 XX
 PT Polypeptide derived from bacterial heat shock protein 65 - for use
 XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 XX rheumatoid arthritis.
 XX
 PS Example 1; Figure 1; 88pp; English.
 XX
 CC AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune

CC diseases such as rheumatoid arthritis.
 XX
 SQ Sequence 15 AA;
 Query Match 53.3%; Score 65; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00075;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 KKWGAPTTNDG 22
 DB 1 KKWGAPTTNDG 12
 RESULT 12
 AAY93331
 ID AAY93331 standard; peptide; 20 AA.
 XX
 AC AAY93331;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of an epitope of heat shock protein 60.
 XX
 KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
 KW inflammatory disorder; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN MO200027870-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 04-NOV-1999; 99MO-IL00595.
 XX
 PR 05-NOV-1998; 98US-0107213.
 XX
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PI Naparstek Y, Ulanovsky R, Kashi Y;
 XX
 DR WPI, 2000-376486/32.
 XX
 DE Peptide having a defined sequence is used in vaccines for conferring
 PT immunity against autoimmune disease or inflammatory disorders,
 PT especially arthritis -
 XX
 PS Claim 4; Page 7; 58pp; English.
 XX
 CC The present sequence represents an epitope of the heat shock
 CC protein 60 (Hsp60) of human origin. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX
 SQ Sequence 20 AA;
 Query Match 48.4%; Score 59; DB 21; Length 20;
 Best Local Similarity 50.0%; Pred. No. 0.011; 3; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 7 VLEKKWGAPTTNDG 22
 DB 2 VLEKKWGAPTTNDG 17
 RESULT 13
 AAU99966
 ID AAU99966 standard; peptide; 20 AA.
 XX
 AC AAU99966;
 XX
 DT 07-OCT-2002 (first entry)

XX
 DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #3.
 XX
 KW Heat shock protein; hsp; hsp60; chronic inflammatory disease;
 KW autoimmune disease; infectious disease; graft rejection; type I diabetes;
 KW juvenile rheumatoid arthritis; multiple sclerosis; cystic;
 KW systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
 KW arteriosclerosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN MO200248312-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 11-DEC-2001; 2001MO-IL01144.
 XX
 PR 11-DEC-2000; 2000IL-0140233.
 XX
 PA (PEPT-) PEPTOR LTD.
 XX
 PI Elias D, Avron A, Senderowitz H;
 XX
 DR WPI, 2002-557613/59.
 XX
 DE New backbone cyclized peptide analog of heat shock protein useful in
 PT the treatment of e.g. autoimmune disease -
 PT
 XX
 PS Claim 5; Page 42; 50pp; English.
 XX
 CC The invention relates to backbone cyclised peptide analogues or
 CC antagonists of heat shock protein (hsp). The analogues and antagonists
 CC are useful in the treatment of chronic inflammatory disease, autoimmune
 CC disease, infectious disease and graft rejection, and for diagnosing
 CC autoimmune and inflammatory disease including juvenile rheumatoid
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide
 CC analogue of a heat shock protein.
 XX
 SQ Sequence 20 AA;
 Query Match 48.4%; Score 59; DB 23; Length 20;
 Best Local Similarity 50.0%; Pred. No. 0.011; 3; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 7 VLEKKWGAPTTNDG 22
 DB 2 VLEKKWGAPTTNDG 17
 RESULT 14
 AAR94778
 ID AAR94778 standard; peptide; 16 AA.
 XX
 AC AAR94778;
 XX
 DT 11-NOV-1996 (first entry)
 XX
 DE Peptide from library spanning whole of hsp65.
 XX
 KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KW prophylaxis.
 XX
 OS Synthetic.
 XX
 PN WO9610039-A1.
 XX
 PD 04-APR-1996.
 XX
 PF 27-SEP-1995; 95MO-GB02295.
 XX

```

PR 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI; 1996-200888/20.
DR
XX Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.
XX
XX Sequence 16 AA;
SQ
Query Match 46.7%; Score 57; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVVLEK 11
DB 6 GPKGRNVVLEK 16
RESULT 15
AAM43456
ID AAM43456 standard; peptide; 16 AA.
XX
XX AAM43456;
AC
XX
XX 08-APR-1998 (first entry)
DT
XX
XX Mycobacteria sp. hsp68 derived peptide (group 1 #6).
DE
XX
XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
KM pristane induced arthritis; PIA.
XX
XX Synthetic.
OS
XX Mycobacteria sp.
OS
XX
XX WO9711966-A1.
PN
XX
XX 03-APR-1997.
PD
XX
XX 26-SEP-1996; 96WO-GB02382.
PF
XX
XX 27-SEP-1995; 95GB-0019737.
PR
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
PA
XX
XX Elson CJ, Thompson JS;
PI
XX
XX WPI; 1997-212851/19.
DR
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
PT for treatment of autoimmune disease esp. arthritis
PT
XX
XX Disclosure; Fig 1a; 91pp; English.
PS
XX
XX This peptide is one of a library (see AAM43451-W43556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study

```

```

CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristane induced arthritis (PIA) in vitro.
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAM1948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.
XX
XX Sequence 16 AA;
SQ
Query Match 46.7%; Score 57; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVVLEK 11
DB 6 GPKGRNVVLEK 16

```

Search completed: December 30, 2003, 16:23:46
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:25:01 ; Search time 31 Seconds

(without alignments)
141.238 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122
Sequence: 1 GPKGRNVLEKKMGAPITTDG 22Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 160453

Minimum DB seq length: 0
Maximum DB seq length: 22Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	90	73.8	16	US-09-847-637B-2	Sequence 2, Appl1
3	87	71.3	16	US-09-847-637B-3	Sequence 3, Appl1
4	59	48.4	20	US-09-847-637B-4	Sequence 4, Appl1
5	36	29.5	20	US-09-847-637B-5	Sequence 5, Appl1
6	35	28.7	19	US-09-847-637B-6	Sequence 6, Appl1
7	35	28.7	20	US-09-847-637B-7	Sequence 7, Appl1
8	35	28.7	20	US-09-847-637B-8	Sequence 8, Appl1
9	35	28.7	20	US-09-847-637B-9	Sequence 9, Appl1
10	35	28.7	20	US-09-847-637B-10	Sequence 10, Appl1
11	34	27.9	14	US-10-323-046-12	Sequence 12, Appl1
12	34	27.9	14	US-10-405-339-5	Sequence 5, Appl1
13	34	27.9	14	US-10-297-229-56	Sequence 56, Appl1
14	34	27.9	14	US-10-106-804B-10	Sequence 10, Appl1
15	34	27.9	14	US-10-106-804B-10	Sequence 10, Appl1

16	34	27.9	17	US-09-769-145-54	Sequence 54, Appl1
17	34	27.9	17	US-09-778-026-14	Sequence 14, Appl1
18	34	27.9	17	US-10-395-032-50	Sequence 50, Appl1
19	34	27.9	17	US-10-006-869-50	Sequence 50, Appl1
20	34	27.9	17	US-10-193-653-68	Sequence 68, Appl1
21	34	27.9	22	US-10-106-804B-20	Sequence 20, Appl1
22	33	27.0	20	US-10-280-066-439	Sequence 439, Appl1
23	32	26.2	9	US-10-228-167A-3	Sequence 3, Appl1
24	32	26.2	12	US-09-753-126-100	Sequence 100, Appl1
25	32	26.2	12	US-09-896-896A-64	Sequence 64, Appl1
26	32	26.2	15	US-09-976-674-61	Sequence 61, Appl1
27	32	26.2	20	US-09-841-137-228	Sequence 228, Appl1
28	32	26.2	9	US-09-841-137-228	Sequence 228, Appl1
29	31.5	25.8	16	US-09-995-587A-33	Sequence 33, Appl1
30	31.5	25.8	16	US-09-995-587A-34	Sequence 34, Appl1
31	31.5	25.8	16	US-09-995-587A-35	Sequence 35, Appl1
32	31.5	25.8	17	US-09-995-587A-36	Sequence 36, Appl1
33	31.5	25.8	17	US-10-128-449A-16	Sequence 16, Appl1
34	31	25.4	13	US-09-852-455-68	Sequence 68, Appl1
35	31	25.4	15	US-10-350-405-5	Sequence 5, Appl1
36	31	25.4	15	US-10-350-405-5	Sequence 5, Appl1
37	31	25.4	15	US-10-121-746-70	Sequence 217, Appl1
38	31	25.4	18	US-09-828-000-6	Sequence 70, Appl1
39	31	25.4	18	US-10-269-806-23	Sequence 23, Appl1
40	31	25.4	18	US-10-269-806-156	Sequence 156, Appl1
41	31	25.4	18	US-10-405-588-6	Sequence 6, Appl1
42	31	25.4	19	US-09-764-872-322	Sequence 322, Appl1
43	30	24.6	14	US-09-805-301-80	Sequence 80, Appl1
44	30	24.6	16	US-10-161-791-228	Sequence 228, Appl1
45	30	24.6	18	US-10-125-669A-15	Sequence 15, Appl1

ALIGNMENTS

RESULT 1
US-09-847-637B-1
Sequence 1, Application US/09847637B
Patent No. US20020150586A1
GENERAL INFORMATION:
APPLICANT: Naparstek, Yaakov
APPLICANT: Umanetsky, Rina
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF
FILE REFERENCE: 13125-002001
CURRENT APPLICATION NUMBER: US/09/847,637B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: PCT/IL99/00595
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,213
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 22
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-1
Query Match
Best Local Similarity 100.0%; Score 122; DB 10; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 GPKGRNVLEKKMGAPITTDG 22
RESULT 2
US-09-847-637B-2
Sequence 2, Application US/09847637B

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; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Ulanovsky, Rina
; APPLICANT: Kashi, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-2

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Best Local Similarity 100.0%; Pred. No. 2,7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-847-637B-3
; Sequence 3, Application US/09847637B
; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
; APPLICANT: Ulanovsky, Rina
; APPLICANT: Kashi, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-3

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLEKKGAPITNDG 22
DB 1 VLEKKGAPITNDG 16

RESULT 4
US-09-847-637B-4
; Sequence 4, Application US/09847637B
; Patent No. US20020150586A1
; GENERAL INFORMATION:
; APPLICANT: Naparstek, Yaakov
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; APPLICANT: Ulanovsky, Rina
; APPLICANT: Kashi, Yechezkel
; TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
; TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
; FILE REFERENCE: 13125-002001
; CURRENT APPLICATION NUMBER: US/09/847,637B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: PCT/IL99/00595
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,213
; PRIOR FILING DATE: 1998-11-05
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; TYPE: PRT
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US-09-847-637B-4

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DB 2 VLEKKGAPITNDG 17

RESULT 5
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; Sequence 44019, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
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OM protein - protein search, using sw model

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Title: US-09-847-637B-1

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 160259

Minimum DB seq length: 0
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Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
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21	34	27.9	17 3 US-08-996-679-63	Sequence 63, Appl
22	34	27.9	17 3 US-08-996-679-63	Sequence 63, Appl
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28	34	27.9	17 4 US-09-839-542B-50	Sequence 50, Appl
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30	33.5	27.5	20 1 US-09-130-287-10	Sequence 10, Appl
31	32	26.2	10 3 US-08-687-590-67	Sequence 67, Appl
32	32	26.2	20 4 US-09-556-877-228	Sequence 228, App
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38	31.5	25.8	17 4 US-08-985-492-16	Sequence 16, Appl
39	31	25.4	9 4 US-09-289-942A-5	Sequence 5, Appl
40	31	25.4	15 4 US-09-336-643A-70	Sequence 70, Appl
41	31	25.4	20 1 US-08-440-861-50	Sequence 50, Appl
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45	30	24.6	16 4 US-09-500-124-228	Sequence 228, App

ALIGNMENTS

RESULT 1
US-08-467-822-11
Sequence 11, Application US/08467822
Patent No. 5843460
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBLACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: HELICOBLACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-822-11

Query Match
Best Local Similarity 29.5%; Score 36; DB 2; Length 8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGRRNV 7
Db 2 GPGRRNV 8

RESULT 2
US-08-432-697-11
Sequence 11, Application US/08432697
Patent No. 6248330
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-432-697-11

Query Match
Best Local Similarity 29.5%; Score 36; DB 3; Length 8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGRRNV 7
Db 2 GPGRRNV 8

RESULT 3
US-08-466-248-11
Sequence 11, Application US/08466248

Patent No. 6258359
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-248-11

Query Match
Best Local Similarity 29.5%; Score 36; DB 3; Length 8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGRRNV 7
Db 2 GPGRRNV 8

RESULT 4
US-08-204-487-4
Sequence 4, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGERU
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIKI

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:29:06 / Search time 13.5 Seconds
(without alignments)
113.978 Million cell updates/sec

Title: US-09-847-637B-2

Sequence: 1 GPKGRNVLEKKMGAP 16

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Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 2770

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	25.6	11	2	A34243	H-hyosopin - Ja
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8	24.4	8	2	A31570	angiotensin-conver
9	23.3	11	2	YHRT	morphogenetic neur
10	23.3	11	2	YHNU	morphogenetic neur
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17	23.3	13	2	150173	alpha-2 collagen -
18	23.3	13	2	A86126	hypothetical prote
19	23.3	13	2	S01904	H+-transporting tw
20	23.3	14	2	S23376	collagen alpha cha
21	23.3	16	2	PH0748	T-cell receptor be
22	22.2	10	2	B53710	ornithine decarbox
23	22.2	10	2	A55695	proteoglycan core
24	22.2	12	2	S65629	protoporphyrinogen
25	22.2	13	2	S04013	lignin peroxidase
26	22.2	13	2	PH0928	T-cell receptor be
27	22.2	14	2	S13864	methyl coenzyme M
28	22.2	14	2	A59018	MUC1 enhancer bind
29	22.2	15	2	T46625	hypothetical prote

30	20	22.2	15	2	D28587	T-cell receptor be
31	20	22.2	16	1	MTDFBS	melanotropin beta
32	20	22.2	16	2	G45681	orf 61.1 - phage T
33	20	22.2	16	2	S36876	aguacobalamun redu
34	19	21.1	11	2	A34662	Achataea cardio-ex
35	19	21.1	11	2	D56979	collagen alpha 1(I
36	19	21.1	13	2	T08533	hypothetical prote
37	19	21.1	13	2	S22995	hypothetical prote
38	19	21.1	13	2	S13273	polyisialoglycoprot
39	19	21.1	13	2	S57567	T cell receptor V-
40	19	21.1	13	2	G83988	hypothetical prote
41	19	21.1	15	2	S21241	oligo-1,6-glucosid
42	19	21.1	15	2	PA0102	fructose-bisphosph
43	19	21.1	16	2	B28587	T-cell receptor be
44	19	21.1	16	2	F53284	T-cell receptor be
45	19	21.1	16	2	PH0767	T-cell receptor be

ALIGNMENTS

RESULT 1
154945
gene C protein - Escherichia coli (fragment)
C/Species: Escherichia coli
C/Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
C/Accession: 154945
R/Tao, T.; Bourne, J.C.; Blumenthal, R.M.
J. Bacteriol. 173, 1367-1375, 1991
A/Title: A family of regulatory genes associated with type II restriction-modification
A/Reference number: 154945; MUID:91139577; PMID:1995588
A/Accession: 154945
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-14 <RES>
A/Cross-references: GB:M63619; NID:G147664; PIDN:AA24555.1; PID:G147665

Query Match 28.9%; Score 26; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RNVLEKK 12
DB 2 KEVIMKK 9

RESULT 2
E58501
25k kidney and gallbladder stone protein - unidentified bacterium (fragment)
C/Species: unidentified bacterium
C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C/Accession: E58501
R/Binette, J.P.; Binette, M.B.
Submitted to the Protein Sequence Database, October 1996
A/Description: The proteins of kidney and gallbladder stones.
A/Reference number: A58501
A/Accession: E58501
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <BIN>
A/Experimental source: human kidney and gallbladder stones
A/Note: tentative identification of 8-Gly and 13-Ser

Query Match 28.9%; Score 26; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KGRNVLEKK 12
DB 6 KGRNVLSKE 15

RESULT 3

MTCMD

melanotropin alpha - Arabian camel

C/Species: Camelus dromedarius (Arabian camel)

C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998

C/Accession: A01464

R/Li, C.H.; Danho, W.O.; Chung, D.; Rao, A.J.

Biochemistry 14, 947-952, 1975

A/Title: Isolation, characterization, and amino acid sequence of melanotropins from camel

A/Reference number: A90393; PMID:75146434; PMID:1125179

A/Accession: A01464

A/Molecule type: protein

A/Residues: 1-13 <LTC>

C/Superfamily: corticotropin-11pocropin

C/Keywords: acetylated amino end; blocked carboxyl end; hormone; pituitary

F/1/Modified site: acetylated amino end (Ser) (partial) #status experimental

F/13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. NO. 9.2e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KMGAP 16

DB 8 RMGKP 12

RESULT 4

MTHOAD

melanotropin alpha - horse

C/Species: Equus caballus (domestic horse)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998

C/Accession: A91785; A01464

R/Dixon, J.S.; Li, C.H.

J. Am. Chem. Soc. 82, 4568-4572, 1960

A/Title: The isolation and structure of alpha-melanocyte-stimulating hormone from horse

A/Reference number: A91785

A/Accession: A91785

A/Molecule type: protein

A/Residues: 1-13 <DIX>

C/Superfamily: corticotropin-11pocropin

C/Keywords: blocked amino end; blocked carboxyl end; hormone; pituitary

F/1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental

F/13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. NO. 9.2e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KMGAP 16

DB 8 RMGKP 12

RESULT 5

JN0730

hypothetical 1.7K protein - phage SPPI

N/Alternate names: hypothetical protein 42.1

C/Species: phage SPPI

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C/Accession: JN0730

R/Chai, S.; Stepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.

Gene 129, 41-49, 1993

A/Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPPI 9

A/Reference number: JN0729; PMID:93328123; PMID:8335255

A/Accession: JN0730

A/Molecule type: DNA

A/Residues: 1-15 <CHA>

A/Cross-references: EMBL:X65941

Query Match 26.7%; Score 24; DB 2; Length 15;

Best Local Similarity 55.6%; Pred. NO. 1.6e+03;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPKGRNVVL 9

DB 5 GPPFRSMVL 13

RESULT 6

A34243

H-hydrophorin - Japanese flounder (fragment)

C/Species: Paralichthys olivaceus (Japanese flounder)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Feb-1999

C/Accession: A34243

R/Seko, A.; Kikajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.

J. Biol. Chem. 264, 15922-15929, 1989

A/Title: Structural studies of fertilization-associated carbohydrate-rich glycoprotein

of a novel penta-antennary N-linked glycan chain in the tandem repeating glycopeptide w

A/Reference number: A34243; PMID:89380184; PMID:2777771

A/Accession: A34243

A/Molecule type: protein

A/Residues: 1-11 <SEK>

A/Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 25.6%; Score 23; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. NO. 1.7e+03;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGRNVVL 10

DB 2 GSVGANTVLD 11

RESULT 7

PH0760

T-cell receptor beta chain (H2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C/Accession: PH0760

R/Cabanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; PMID:9207846; PMID:1836010

A/Accession: PH0760

A/Molecule type: mRNA

A/Residues: 1-15 <CAB>

A/Cross-references: EMBL:X60855; NID:951194; PIDN:CAA43245.1; PID:951195

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match 25.6%; Score 23; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. NO. 2.3e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKGRN 6

DB 5 PGRN 9

RESULT 8

A31570

angiotensin-converting enzyme inhibitor - yellowfin tuna

C/Species: Thunnus albacares (yellowfin tuna)

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000

C/Accession: A31570

R/Kobama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.

Biochem. Biophys. Res. Commun. 155, 332-337, 1988

A/Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.

A/Reference number: A31570; PMID:88326322; PMID:3415688

A/Accession: A31570

A/Molecule type: protein

A/Residues: 1-8 <KOH>

A/Note: The source is designated as Neothunnus macropterus

C/Superfamily: unassigned animal peptides

C/Keywords: angiotensin-converting enzyme inhibitor

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:26:11 ; Search time 10 Seconds
(without alignments)
75.243 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVVLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 872

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	27.8	13	MLA_ANOCA	P41589 anolis caro
2	25	27.8	13	MLA_ANOCA	P01198 camelus dro
3	22	24.4	8	ACT_THUL	P18691 chunnus alb
4	21	23.3	11	MORN_HUMAN	P01163 homo saplen
5	20	22.2	13	LIGA_TRAVS	P20011 tremeetes ve
6	20	22.2	14	MCRX_METTM	P58815 methanobact
7	20	22.2	16	MLB_SQUAC	P01207 equalus aca
8	19	21.1	9	TKLI_LOCM1	P16223 locusta mig
9	19	21.1	11	CEPI_ACHFU	P22790 achnatna fu
10	19	21.1	12	UP01_CABETL	P55954 caenothabdi
11	19	21.1	13	IDHP_RAT	P56574 rattus norv
12	19	21.1	15	UC06_MAIZE	P80612 zea mays (m
13	19	21.1	16	NMPX_SOLTU	P80501 solanum tub
14	18	20.0	9	CONO_CONGR	P03486 conus geogr
15	18	20.0	10	BPP8_BOTIN	P30426 bochrops in
16	18	20.0	10	BPP_VIPAS	P31351 vipera aspi
17	18	20.0	12	PSB3_PHYPA	P80662 physcomitre
18	18	20.0	12	RPI_CONSP	P58805 conus spuri
19	18	20.0	13	PSBF_PINPS	P18668 pinus pinas
20	18	20.0	14	TAT_HVIW2	P15052 human immun
21	18	20.0	15	TAT_HVI18	P80072 bacillus th
22	18	20.0	15	MLAT_BACTQ	P30425 bochrops in
23	17.5	19.4	5	BPP7_BOTIN	P13737 mytilus edu
24	17	18.9	6	CTP2_MYTED	P41491 locusta mig
25	17	18.9	6	LOKI_LOCM1	P21140 leucophaea
26	17	18.9	8	LCK1_LEUMA	P21141 leucophaea
27	17	18.9	8	LCK2_LEUMA	P21142 leucophaea
28	17	18.9	8	LCK3_LEUMA	P21143 leucophaea
29	17	18.9	8	LCK4_LEUMA	P19987 leucophaea
30	17	18.9	8	LCK5_LEUMA	P19988 leucophaea
31	17	18.9	8	LCK6_LEUMA	P19989 leucophaea
32	17	18.9	8	LCK7_LEUMA	P19990 leucophaea
33	17	18.9	8	LCK8_LEUMA	

34	17	18.9	8	1	RT34_BOVIN	P82929 bos taurus
35	17	18.9	9	1	FAR6_MACRS	P83279 macrobrachi
36	17	18.9	9	1	SAP_STOVA	P24047 stomopneute
37	17	18.9	10	1	FAR6_PANRE	P82660 panagrellus
38	17	18.9	10	1	HTF1_ROMMI	P18110 romalea mic
39	17	18.9	10	1	HTF2_CARMO	P13185 carausius m
40	17	18.9	10	1	HTF_FELZE	P16353 heliothis z
41	17	18.9	10	1	HTF_NAUCI	P10939 nauphoeta c
42	17	18.9	10	1	HTF_TABAT	P14596 tabanus atr
43	17	18.9	10	1	LABA_JATMU	P13270 jatropha mu
44	17	18.9	10	1	TPIS_NICPL	P19118 nicotiana p
45	17	18.9	12	1	H2AX_ONCMW	P83327 oncorhynch

ALIGNMENTS

```

RESULT 1
MLA_ANOCA STANDARD; PRT; 13 AA.
AC P41589;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Anolis carolinensis (Green anole) (American chameleon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxId=28377;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary; PubMed=167689;
RX MEDLINE=92270473;
RA Dorez R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;
RT "Detection of a novel sequence change in the major form of alpha-MSH
RT isolated from the intermediate pituitary of the reptile, Anolis
RT carolinensis."
RL Peptides 12:1261-1266(1991).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR InterPro: IPR001941; Mcoortin ACTH.
DR Pfam: PF00976; ACTH_domain; I.
KW Hormone; Amidation.
FT MOD_RES 13
FT SEQUENCE 13 AA; 1608 MW; FP990A7358B09C1 CRC64;
SQ
Query Match 27.8%; Score 25; DB 1; Length 13;
Query Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 KWGAP 16
DB 8 RWGAP 12
RESULT 2
MLA_CAMDR STANDARD; PRT; 13 AA.
AC P01198;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Camelus dromedarius (Dromedary) (Arabian camel), and
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxId=9838, 9796;
RN [1]
RP SEQUENCE.
RC SPECIES=C.dromedarius;
RX MEDLINE=7514634; PubMed=1125179;
RA Li C.H., Danto W.O., Chung D., Rao A.J.;
RT "Isolation, characterization, and amino acid sequence of

```

Rt	melanotropins from camel pituitary glands.";					
Rl	Biochemistry 14:947-952(1975).					
Rn	[2]					
Rp	SEQUENCE.					
Rc	SPECIES=Horse; TISSUE=Pituitary;					
Ra	Dixon J.S., Li C.H.;					
Rt	"The isolation and structure of alpha-melanocyte-stimulating hormone					
Rr	from horse pituitaries";					
Rl	J. Am. Chem. Soc. 82:4568-4572 (1960).					
Cc	-I- SIMILARITY: BELONGS TO THE POMC FAMILY.					
Dr	PIR; A01464; MTHOAD.					
DR	PIR; A91785; MTHOAD.					
DR	InterPro; IPR001941; Mcortin ACTH.					
KM	Pfam; PF00976; ACTH domain; I.					
FT	Hormone; Acetylation; Amidation.					
FT	MOD_RES	1				
FT			1			
FT	MOLECULES).					
FT	AMIDATION.					
SQ	SEQUENCE	13 AA;	1624 MW;	PF991CA958BB09C1 CRC64;		
Oy	Query Match	27.8%;	Score 25;	DB 1;	Length 13;	
	Best Local Similarity	60.0%;	Pred. No. 5.5e+02;			
	Matches	3;	Conservative	1;	Mismatches	1;
					Indels	0;
					Gaps	0;
Db	12 KWGP	16				
	:	:	:			
	8 RWGKP	12				
	RESULT 3					
	ACI_THUHL					
ID	_ACI_THUHL	STANDARD;	PRT;	8 AA.		
Ac	P18691;					
Dt	01-NOV-1990 (Rel. 16; Created)					
Dt	01-NOV-1990 (Rel. 16; Last sequence update)					
Dt	01-NOV-1990 (Rel. 16; Last annotation update)					
DE	Angiotensin-converting enzyme inhibitor					
OS	Thunnus albacares (Yellowfin tuna) (Neotunus macropterus).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;					
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;					
OC	Acanthomorphia; Neopterygii; Perciformes; Perculiformes; Scombroidei;					
OC	Scombridae; Thunnus.					
XN	NCBI_Taxid=8236;					
RP	[1]					
RP	SEQUENCE.					
RC	TISSUE=Muscle;					
RC	MEDLINE=88326322; PubMed=3415688;					
RA	Kohama Y., Matsuno S., Oka H., Teramoto T., Okabe M., Mimura T.;					
Rt	"Isolation of angiotensin-converting enzyme inhibitor from tuna					
Rt	muscle.";					
RL	Biochem. Biophys. Res. Commun. 155:332-337(1988).					
DR	PIR; A31570; A31570.					
SQ	SEQUENCE	8 AA;	953 MW;	6AA863733051F1B7 CRC64;		
	Query Match	24.4%;	Score 22;	DB 1;	Length 8;	
	Best Local Similarity	100.0%;	Fred. NO. 1.3e+05;			
	Matches	3;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0;
Oy	12 KWGP	14				
	:	:				
Db	5 KWGP	7				
	RESULT 4					
	MORN_HUMAN					
ID	_MORN_HUMAN	STANDARD;	PRT;	11 AA.		
AC	F01163;					
Dt	21-JUL-1986 (Rel. 01; Created)					
Dt	21-JUL-1986 (Rel. 01; Last sequence update)					
Dt	28-FEB-2003 (Rel. 41; Last annotation update)					
DE	Morphogenetic neuromer peptide (Head activator) (HA).					
OS	Homo sapiens (Human);					
OS	Rattus norvegicus (Rat);					

```

05 Bos taurus (Bovine);
06 Anthopleura elegantissima (Sea anemone), and
07 Hydra attenuata (Hydra) (Hydra vulgaris).
08 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
09 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
10 NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
11
12 SEQUENCE.
13 SPECIES=Human, Rat, and Bovine;
14 MEDLINE=82035850; PubMed=7290191.
15 RA Bodemuller H.C., Schaller H.C.;
16 "Conserved amino acid sequence of a neuropeptide, the head activator,
17 from coelenterates to humans.";
18 Nature 293:579-580(1981).
19
20 SEQUENCE.
21 SPECIES=A.elegantissima, and H.attenuata;
22 Schaller H.C., Bodemuller H.;
23 "Isolation and amino acid sequence of a morphogenetic peptide from
24 hydra.";
25 Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
26
27 SYNTHESIS.
28 MEDLINE=82050803; PubMed=7297679;
29 Bitt C., Zachmann B., Bodemuller H., Schaller H.C.;
30 "Synthesis of a new neuropeptide, the head activator from hydra.";
31 FEBS Lett. 131:317-321(1981).
32
33 FUNCTION.
34 MEDLINE=90059923; PubMed=2583101;
35 Schaller H.C., Druffel-Augustin S., Dubel S.;
36 "Head activator acts as an autocrine growth factor for NH15-CA2 cells
37 in the G2/mitosis transition.";
38 EMBO J. 8:3311-3318(1989).
39
40 -1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
41 IN THE G2/MITOSIS TRANSITION.
42
43 -1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
44 AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
45 HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
46 BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
47
48 PIR; A01427; YHRT.
49 PIR; A93900; YHXA.
50 PIR; B01427; YHHU.
51 PIR; B93900; YHJFHY.
52 PIR; C01427; YHBO.
53
54 DR GK; P01163; "-
55 Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
56 MOD RSS 1 1 PYRROLIDONE CARBOXYLIC ACID.
57 FT 1 1
58 SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;
59
60 Query Match 23.3%; Score 21; DB 1; Length 11;
61 Best Local Similarity 50.0%; Pred. No. 2;le+03;
62 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
63
64 QY 2 PKGRNVLT 9
65 | | | | |
66 DB 3 PGSGKSVLT 10
67
68 RESULT 5
69 LIGA TRAVE STANDARD; PRT; 13 AA.
70 AC P20011;
71 DT 01-FEB-1991 (Rel. 17, Created)
72 DT 01-FEB-1991 (Rel. 17, Last sequence update)
73 DT 28-FEB-2003 (Rel. 41, Last annotation update)
74 DB Ligninase A (EC 1.11.1.14) (diarylpropane peroxidase) (Lignin
75 peroxidase) (Pregment).
76 OS Trameetes versicolor (White-rot fungus).
77 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
78 Abhylophorales; Trameetes.
79 NCBI_TaxID=5325;
80
81 [1]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:29:41 ; Search time 28 Seconds
(without alignments)
147,459 Million cell updates/sec

Title: US-09-847-637B-2

Sequence: 1 GPKGRNVVLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4022

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL.23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	28.9	14	2	Q47599
2	25	27.8	10	11	O70580
3	24	26.7	10	4	O9UNF2
4	24	26.7	15	2	O9RAP5
5	23	25.6	11	15	O83410
6	23	25.6	13	15	O85645
7	23	25.6	16	4	O9UC18
8	23	25.6	16	8	O9T2V8
9	23	25.6	16	10	O9S8D6
10	22	24.4	14	10	O9RS17
11	22	24.4	14	10	P82322
12	21.5	23.9	13	5	O9WS06
13	21	23.3	8	8	O94PX5
14	21	23.3	8	8	O94VB2
15	21	23.3	8	8	O94PX7
16	21	23.3	8	8	O94PX6

17	21	23.3	8	8	Q94VA7	Q94V27	varanus sal
18	21	23.3	8	8	Q94VB5	Q94VB5	varanus sal
19	21	23.3	9	8	Q94VC6	Q94VC6	varanus pil
20	21	23.3	10	8	Q94VD5	Q94VD5	varanus pil
21	21	23.3	12	7	O31006	O31006	bos taurus
22	21	23.3	13	7	O9TNO8	O9TNO8	homo sapien
23	21	23.3	13	8	O9MOKO	O9MOKO	cervus elap
24	21	23.3	13	8	O9MOK6	O9MOK6	rupicapra r
25	21	23.3	13	8	O9MOK3	O9MOK3	capra ibex
26	21	23.3	13	16	O8X4F5	O8X4F5	escherichia
27	21	23.3	15	4	O9BXK4	O9BXK4	homo sapien
28	21	23.3	15	8	O92076	O92076	homo sapien
29	21	23.3	15	5	O9TWS8	O9TWS8	euhadra her
30	21	23.3	16	5	O9TWS8	O9TWS8	lamellibrac
31	21	23.3	16	5	O9TWS8	O9TWS8	trypanosoma
32	20	22.2	8	4	O16468	O16468	homo sapien
33	20	22.2	10	2	O9R7J8	O9R7J8	helicobacte
34	20	22.2	10	11	O63389	O63389	rattus norv
35	20	22.2	11	2	O9EUB3	O9EUB3	escherichia
36	20	22.2	11	15	O9ADI8	O9ADI8	human immun
37	20	22.2	12	4	O9UMQ9	O9UMQ9	homo sapien
38	20	22.2	12	4	O9H4X3	O9H4X3	homo sapien
39	20	22.2	12	15	O8ODY5	O8ODY5	human immun
40	20	22.2	12	15	O8ODY4	O8ODY4	human immun
41	20	22.2	12	15	O8ODY4	O8ODY4	human immun
42	20	22.2	12	15	O8ODY4	O8ODY4	human immun
43	20	22.2	12	15	O8ODY4	O8ODY4	human immun
44	20	22.2	12	15	O8ODY4	O8ODY4	human immun
45	20	22.2	12	15	O8ODY6	O8ODY6	human immun

ALIGNMENTS

RESULT 1

Q47599 PRELIMINARY; PRT; 14 AA.
AC Q47599;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE C (Fragment).
GN C.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
modification systems".
RL J. Bacteriol. 173:1367-1375 (1991).
DR EMBL; M63619; AAA2455.1; -.
FT NON TER
SQ SEQUENCE 14 AA; 1705 MW; 77B6CA60581A4F3B CRC64;

Query Match 28.9%; Score 26; DB 2; Length 14;
Best local similarity 50.0%; Pred. NO. 1.5e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RNVVLEKK 12
Db 2 KEVIMEKK 9

RESULT 2

O70580 PRELIMINARY; PRT; 10 AA.
AC O70580;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE Carbonic anhydrase III (Fragment).
 GN CAR3 OR CAR3 OR CA3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sowden J., Smith H., Morrison K., Edwards Y.;
 RT "Sequence comparisons and functional studies of the proximal promoter
 of the carbonic anhydrase 3 (CA3) gene.";
 RL Gene 214:157-165(1999).
 DR EMBL; AJ006474; CAA07057.1; -.
 DR MGI; MGI:88270; Car3.
 DR MGD; MGI:1351477; Car3.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1105 MW; 567FE71ADC37B13 CRC64;

Query Match 26.7%; Score 24; DB 11; Length 10;
 Best Local Similarity 37.5%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 9 LEKKGAP 16
 DB 1 MAKEWATP 8

RESULT 3
 O9UNF2 PRELIMINARY; PRT; 10 AA.
 AC O9UNF2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DE 01-MAY-2000 (TrEMBLrel. 13, last annotation update)
 DE Alpha 1 collagen (Fragment).
 GN COL1A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RA Ratcliffe T.A., Vitz J.R., Ray D.B.;
 RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene
 at 10,828 bp: cytosine replaces adenine.";
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF128441; AAD32608.1; -.
 KW Collagen.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 953 MW; 364F91A873276867 CRC64;

Query Match 26.7%; Score 24; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKG 4
 DB 4 GPKG 7

RESULT 4
 O9R4P5 PRELIMINARY; PRT; 15 AA.
 AC O9R4P5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, last annotation update)
 DE Ribosomal protein L24 (Fragment).
 OS Brevundimonas diminuta (Pseudomonas diminuta).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;

OC Caulobacteraceae; Brevundimonas.
 OX NCBI_TaxId=293;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95244309; Pubmed=7727274;
 RA Ochi K.;
 RT "Comparative ribosomal protein sequence analyses of a phylogenetically
 RT defined genus, Pseudomonas, and its relatives.";
 RL Int. J. Syst. Bacteriol. 45:268-273(1995).
 SQ SEQUENCE 15 AA; 1513 MW; 8BA258CFA725914F CRC64;

Query Match 26.7%; Score 24; DB 2; Length 15;
 Best Local Similarity 71.4%; Pred. No. 3.5e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KGRNVVL 9
 DB 6 KGRNVVL 12

RESULT 5
 O83410 PRELIMINARY; PRT; 11 AA.
 AC O83410;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Superantigen (Fragment).
 GN SAG.
 OS Mouse mammary tumor virus.
 OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
 OX NCBI_TaxId=11757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mtv-6.
 RX MEDLINE=55133174; Pubmed=7831795;
 RA Cho K., Ferrick D.A., Morris D.W.;
 RT "Structure and biological activity of the subgenomic Mtv-6 endogenous
 RT provirus.";
 RL Virology 206:395-402(1995).
 DR EMBL; L37518; AAA66963.1; -.
 DR InterPro; IPR001213; MMTV_SAG.
 DR Pfam; PF01054; MMTV_SAG; 1.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1401 MW; 5B6B080A7326C6D7 CRC64;

Query Match 25.6%; Score 23; DB 15; Length 11;
 Best Local Similarity 60.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 9 LEKKM 13
 DB 4 LQCKM 8

RESULT 6
 O85645 PRELIMINARY; PRT; 13 AA.
 AC O85645;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Endogenous mouse mammary tumor virus proviral LTR gene product, 5' end
 DE (Fragment).
 OS Mouse mammary tumor virus.
 OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
 OX NCBI_TaxId=11757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83138005; Pubmed=6298469;
 RA Wheeler D.A., Butel J.S., Medina D., Cardiff R.D., Hager G.L.;
 RT "Transcription of mouse mammary tumor virus: Identification of a
 RT candidate mRNA for the long terminal repeat gene product.";

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:25:36 ; Search time 35 Seconds

(without alignments)
72.561 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVVLEKMKCAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 360314

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_19Jun03:.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90	100.0	16	21	AAV93329	Amino acid sequence
2	90	100.0	16	23	AAU99966	Mycobacterium tube
3	83	92.2	15	17	AAK94779	Peptide from libra
4	83	92.2	15	18	AAW43457	Mycobacteriella sp. h
5	61	67.8	16	17	AAK94780	Peptide from libra
6	61	67.8	16	18	AAW43458	Mycobacteriella sp. h
7	57	63.3	16	17	AAK94778	Peptide from libra
8	57	63.3	16	18	AAW43456	Mycobacteriella sp. h
9	55	61.1	16	21	AAV93330	Amino acid sequence

10	55	61.1	16	23	AAU99965	Mycobacterium tube
11	47	52.2	11	22	AAK88272	Hsp-65 peptide epi
12	43	47.8	10	22	AAK88269	Hsp-65 peptide epi
13	39	43.3	9	22	AAK88279	Peptide from libra
14	38	42.2	15	17	AAK94781	Mycobacteriella sp. h
15	38	42.2	15	18	AAW43459	Mycobacteriella sp. h
16	34	37.8	14	21	AAK10751	Fibrin gel binding
17	34	37.8	14	21	AAK10756	Proteoglycan bindi
18	34	37.8	14	22	AAK35931	NCAW/heparin bindi
19	34	37.8	14	23	AAU85712	Neural cell adhesi
20	34	37.8	14	23	AAU50288	Cytochrome b12 N-t
21	34	37.8	15	22	AAK64059	G. multiflorum rec
22	32	35.6	16	22	ABG71559	Melanocyte stimula
23	31	34.4	12	22	AAK90858	Tie-1 binding surr
24	31	34.4	13	23	AAK48084	Human secreted pro
25	30	33.3	14	18	AAK32456	Delivery peptide u
26	30	33.3	14	18	AAK38766	Nucleic acid (NA)
27	30	33.3	14	18	AAW24451	Gb2 N-terminal SH
28	30	33.3	15	18	AAK25443	Hepatitis C virus
29	29.5	32.8	15	19	AAK37382	G protein-coupled
30	29.5	32.8	16	24	ABP62686	Molt-4 leukaemia c
31	29	32.2	7	23	ABJ04516	Nuclear localisati
32	29	32.2	9	22	AAK45892	Compressing peptid
33	29	32.2	13	17	AAK86962	Human procathepsin
34	29	32.2	13	18	AAK19794	Human procathepsin
35	29	32.2	13	23	ABK97728	Human procathepsin
36	29	32.2	13	23	ABK97729	Human procathepsin
37	29	32.2	14	22	AAK97155	Human procathepsin
38	29	32.2	14	22	AAK00717	Human procathepsin
39	29	32.2	14	23	ABG66058	Human procathepsin
40	29	32.2	15	19	AAK75543	Collagen II specif
41	29	32.2	15	23	ABG61615	Human DPER-3 pepti
42	28.5	31.7	10	22	AAK94842	Human complementar
43	28	31.1	9	19	AAK56753	A. tumefaciens ant
44	28	31.1	9	22	AAU02332	H1A binding TADG-1
45	28	31.1	12	18	AAK38002	WW domain binding

ALIGNMENTS

RESULT 1	AAV93329	standard; peptide; 16 AA.
ID	AAV93329	
XX	AAV93329;	
AC	04-SEP-2000	(first entry)
XX		
DT		
DE		Amino acid sequence of an epitope of heat shock protein 60.
DE		Epitope; heat shock protein 60; Hep60; vaccine; autoimmune disease;
KW		inflammatory disorder; arthritis.
KW		
XX		
OS		Mycobacterium tuberculosis.
XX		
PN		W0200027870-A1.
XX		
PD		18-MAY-2000.
XX		
XX		
PF		04-NOV-1999; 99WO-IL00595.
XX		
PR		05-NOV-1998; 98US-0107213.
XX		
PA		(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX		
XX		Naparetek Y, Ulimansky R, Kaashi Y;
XX		
DR		WPI; 2000-376486/32.
XX		
XX		Peptide having a defined sequence is used in vaccines for conferring
PT		immunity against autoimmune disease or inflammatory disorders,
PT		especially arthritis -

XX Claim 2, Page 7, 58pp; English.
 PS
 CC The present sequence represents an epitope of the heat shock protein
 CC 60 (hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 90; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVLEKKWGAP 16
 DB 1 GPKGRNVLEKKWGAP 16
 RESULT 2
 AAU99964 standard; Peptide: 16 AA.
 AAU99964;
 07-OCT-2002 (first entry)
 Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.
 DE
 XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;
 XX autoimmune disease; infectious disease; graft rejection; type I diabetes;
 KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
 KM systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
 KM arteriosclerosis.
 XX
 OS Mycobacterium tuberculosis.
 OS
 XX WO200248312-A2.
 PN 20-JUN-2002.
 PD 11-DEC-2001; 2001WO-1101144.
 PF 11-DEC-2000; 2000IL-0140233.
 PR (PEPT-) PEPTOR LTD.
 PA Elias D, Avron A, Senderowitz H;
 PI WPI; 2002-557613/59.
 DR
 XX New backbone cyclised peptide analog of heat shock protein useful in
 PT the treatment of e.g. autoimmune disease -
 PT
 XX Claim 5; Page 42; 50pp; English.
 PS
 XX The invention relates to backbone cyclised peptide analogues or
 CC antagonists of heat shock protein (hsp). The analogues and antagonists
 CC are useful in the treatment of chronic inflammatory disease, autoimmune
 CC disease, infectious disease and graft rejection, and for diagnosing
 CC autoimmune and inflammatory disease including juvenile rheumatoid
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide
 CC analogue of a heat shock protein.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 90; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16
 DB 1 GPKGRNVLEKKWGAP 16
 RESULT 3
 AAR94779 standard; peptide: 15 AA.
 AAR94779;
 11-NOV-1996 (first entry)
 Peptide from library spanning whole of hsp65.
 DE
 XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
 KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KM prophylaxis.
 KM
 XX Synthetic.
 OS
 XX WO9610039-A1.
 PN 04-APR-1996.
 PD 27-SEP-1995; 95WO-GB02295.
 XX 27-SEP-1994; 94GB-0019553.
 XX 27-SEP-1994; 94GB-0019553.
 PR (PEPT-) PEPTIDE THERAPEUTICS LTD.
 PA Elson CJ, Thompson SJ;
 PI WPI; 1996-200888/20.
 DR
 XX Polypeptide derived from bacterial heat shock protein 65 - for use
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 PT rheumatoid arthritis.
 PT
 XX Example 1, Figure 1, 88pp; English.
 PS
 XX AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides conrg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 92.2%; Score 83; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVLEKKWGA 15
 DB 1 GPKGRNVLEKKWGA 15
 RESULT 4
 AAM43457 standard; peptide: 15 AA.
 AAM43457;
 08-APR-1998 (first entry)
 Mycobacteria sp. hsp68 derived peptide (group 1 #7).

KM Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM pristane induced arthritis; PIA.
 OS Synthetic.
 OS Mycobacteria sp.
 PN WO9711966-A1.
 XX
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-GB02382.
 XX
 PR 27-SEP-1995; 95GB-0019737.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
 XX
 PI Elson CJ, Thompson JS;
 XX
 DR WPI, 1997-212851/19.
 XX
 PT Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis
 XX
 PS Disclosure; Fig 1a; 91pp; English.
 XX
 CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW43458-W43950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.
 CC
 SQ Sequence 15 AA;
 Query Match 92.2%; Score 83; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVLEKKWGA 15
 DB 1 GPKGRNVLEKKWGA 15
 RESULT 5
 AAR94780
 ID AAR94780 standard; peptide; 16 AA.
 XX
 AC AAR94780;
 XX
 DT 11-NOV-1996 (first entry)
 XX
 DE Peptide from library spanning whole of hsp65.
 XX
 KM Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM prophylaxis.
 XX
 OS Synthetic.
 XX
 PN WO9610039-A1.
 XX
 PD 04-APR-1996.
 XX
 PF 27-SEP-1995; 95WO-GB02295.
 XX

PR 27-SEP-1994; 94GB-0019553.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Elson CJ, Thompson SJ;
 XX
 DR WPI, 1996-200888/20.
 XX
 XX Polypeptide derived from bacterial heat shock protein 65 - for use
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 PT rheumatoid arthritis.
 XX
 PS Example 1; Figure 1; 88pp; English.
 XX
 CC AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.
 XX
 SQ Sequence 16 AA;
 Query Match 67.8%; Score 61; DB 17; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 NVYLEKKWGAP 16
 DB 1 NVYLEKKWGAP 11
 RESULT 6
 AAW43458
 ID AAW43458 standard; peptide; 16 AA.
 XX
 AC AAW43458;
 XX
 DT 08-APR-1998 (first entry)
 XX
 DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).
 XX
 KM Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM pristane induced arthritis; PIA.
 XX
 OS Synthetic.
 OS Mycobacteria sp.
 PN WO9711966-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-GB02382.
 XX
 PR 27-SEP-1995; 95GB-0019737.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
 XX
 PI Elson CJ, Thompson JS;
 XX
 DR WPI, 1997-212851/19.
 XX
 PT Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis
 XX
 PS Disclosure; Fig 1a; 91pp; English.
 XX
 CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study

CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW4948-W4950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.

XX Sequence 16 AA;

Query Match 67.8%; Score 61; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVVLEKRWGAP 16
 |||||
 1 NVVLEKRWGAP 11

RESULT 7

AAW434778 AAW434778 standard; peptide; 16 AA.

XX AAW434778;

XX 11-NOV-1996 (first entry)

DE Peptide from library spanning whole of hsp65.

KM Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
 KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KM prophylaxis.

OS Synthetic.

PN W09610039-A1.

PD 04-APR-1996.

PF 27-SEP-1995; 95WO-GB02295.

PR 27-SEP-1994; 94GB-0019553.

PA (2BPT-) PEPTIDE THERAPEUTICS LTD.

PI Elson CJ, Thompson SJ;

XX WPI; 1996-200888/20.

PT Polypeptide derived from bacterial heat shock protein 65 - for use
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 PT rheumatoid arthritis.

XX Example 1; Figure 1; 88pp; English.

CC AAW4773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAW4772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.

XX Sequence 16 AA;

Query Match 63.3%; Score 57; DB 17; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0062;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEK 11
 |||||
 6 GPKGRNVVLEK 16

RESULT 8

AAW43456 AAW43456 standard; peptide; 16 AA.

XX AAW43456;

XX 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #6).

KM Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM pristane induced arthritis; PIA.

OS Synthetic.

OS Mycobacteria sp.

PN W09711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (2BPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

XX WPI; 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis

PS Disclosure; Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW4948-W4950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.

XX Sequence 16 AA;

Query Match 63.3%; Score 57; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0062;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVVLEK 11
 |||||
 6 GPKGRNVVLEK 16

RESULT 9

AAW43330 AAW43330 standard; peptide; 16 AA.

XX AAW43330;

XX 04-SEP-2000 (first entry)
 DT Amino acid sequence of an epitope of heat shock protein 60.
 XX
 DE Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
 XX inflammatory disorder; arthritis.
 KM
 XX Mycobacterium tuberculosis.
 OS
 XX WO200027870-A1.
 PN
 XX 18-MAY-2000.
 PD
 XX 04-NOV-1999; 99WO-IL00595.
 PF
 XX 05-NOV-1998; 98US-0107213.
 PR
 XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA
 XX Naparetek Y, Ulmansky R, Kaashi Y;
 PI
 XX WPI; 2000-376486/32.
 DR
 XX Peptide having a defined sequence is used in vaccines for conferring
 PT immunity against autoimmune disease or inflammatory disorders,
 PT especially arthritis -
 PS
 XX Claim 3; Page 7; 58pp; English.
 PS
 XX The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 CC
 SQ Sequence 16 AA;
 QY
 DB 7 VVLEKKWGAP 16
 1 VVLEKKWGAP 10
 RESULT 10
 AAU99965
 ID AAU99965 standard; Peptide; 16 AA.
 XX
 AC AAU99965;
 DT 07-OCT-2002 (first entry)
 DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.
 XX
 KM Heat shock protein; hsp; hsp60; chronic inflammatory disease;
 KM autoimmune disease; infectious disease; graft rejection; type I diabetes;
 KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
 KM systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
 KM arteriosclerosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200248312-A2.
 PD 20-JUN-2002.
 PF 11-DEC-2001; 2001MO-IL01144.
 PR 11-DEC-2000; 2000IL-0140233.

XX (PEPT-) PEPTOR LTD.
 PA
 XX Elias D, Avron A, Senderowitz H;
 PI
 XX WPI; 2002-557613/59.
 DR
 XX New backbone cyclized peptide analog of heat shock protein useful in
 PT the treatment of e.g. autoimmune disease -
 PT
 XX Claim 5; Page 42; 50pp; English.
 PS
 XX The invention relates to backbone cyclised peptide analogues or
 CC antagonists of heat shock protein (hsp). The analogues and antagonists
 CC are useful in the treatment of chronic inflammatory disease, autoimmune
 CC disease, infectious disease and graft rejection, and for diagnosing
 CC autoimmune and inflammatory disease including juvenile rheumatoid
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide
 CC analogue of a heat shock protein.
 CC
 SQ Sequence 16 AA;
 QY
 DB 7 VVLEKKWGAP 16
 1 VVLEKKWGAP 10
 RESULT 11
 AAB88272
 ID AAB88272 standard; Peptide; 11 AA.
 XX
 AC AAB88272;
 DT 17-MAY-2001 (first entry)
 DE Hsp-65 peptide epitope #46.
 XX
 KM Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;
 KM immune response inducer; vaccine; gene therapy; bacterial infection;
 KM tuberculosis.
 XX
 OS Mycobacterium sp.
 XX
 PN WO200116174-A2.
 PD 08-MAR-2001.
 PF 30-AUG-2000; 2000WO-IB01326.
 PR 30-AUG-1999; 99US-0151396.
 XX
 PA (KTES/) KTESLING R.
 PA (CHAR/) CHARO J M.
 PA (OTEN/) OTENHOFF T H M.
 PA (GELU/) GELUK A.
 XX
 PI Ktesling R, Charo JM, Otenhoff THM, Geluk A;
 XX
 DR WPI; 2001-244396/25.
 DT Novel polypeptides containing epitopes derived from Mycobacterial heat
 PT shock protein 65 useful for treating bacterial and parasitic
 PT infections, such as tuberculosis -
 PS Disclosure; Page 55; 117pp; English.
 CC The present sequence is a peptide epitope derived from Mycobacterial heat

CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.
 CC Mycobacterium e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
 CC is useful for treating bacterial and parasitic infections such as
 CC tuberculosis.
 CC
 SQ Sequence 11 AA;
 Query Match 52.2%; Score 47; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVVL 9
 DB 3 GPKGRNVVL 11
 RESULT 12
 AAB88269
 ID AAB88269 standard; Peptide; 10 AA.
 AC AAB88269;
 XX
 XX
 DT 17-MAY-2001 (first entry)
 DE Hsp-65 peptide epitope #43.
 XX
 XX
 DE Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;
 KW immune response inducer; vaccine; gene therapy; bacterial infection;
 KM tuberculosis.
 KM
 KM Mycobacterium sp.
 XX
 XX
 OS WO200116174-A2.
 XX
 PN 08-MAR-2001.
 XX
 PD 30-AUG-2000; 2000WO-IB01326.
 PF 30-AUG-1999; 99US-0151396.
 XX
 PR 30-AUG-1999; 99US-0151396.
 XX
 PA (KIES/) KIESSLING R.
 PA (CHAR/) CHARO J M.
 PA (OTEN/) OTENHOFF T H M.
 PA (GELU/) GELUK A.
 XX
 PI Kieselring R, Charo JM, Otenhoff TM, Geluk A;
 PI
 DR WPI; 2001-244396/25.
 XX
 DR Novel polypeptides containing epitopes derived from Mycobacterial heat
 PT shock protein 65 useful for treating bacterial and parasitic
 PT infections, such as tuberculosis -
 XX
 XX
 PS Disclosure; Page 55; 117pp; English.
 XX
 XX The present sequence is a peptide epitope derived from Mycobacterial heat
 CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.
 CC Mycobacterium e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
 CC is useful for treating bacterial and parasitic infections such as

CC tuberculosis.
 XX
 SQ Sequence 10 AA;
 Query Match 47.8%; Score 43; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNV 8
 DB 3 GPKGRNV 10
 RESULT 13
 AAB88279
 ID AAB88279 standard; Peptide; 9 AA.
 AC AAB88279;
 XX
 XX
 DT 17-MAY-2001 (first entry)
 DE Hsp-65 peptide epitope #53.
 XX
 XX
 DE Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;
 KW immune response inducer; vaccine; gene therapy; bacterial infection;
 KM tuberculosis.
 KM
 KM Mycobacterium sp.
 XX
 XX
 OS WO200116174-A2.
 XX
 PN 08-MAR-2001.
 XX
 PD 30-AUG-2000; 2000WO-IB01326.
 PF 30-AUG-1999; 99US-0151396.
 XX
 PR 30-AUG-1999; 99US-0151396.
 XX
 PA (KIES/) KIESSLING R.
 PA (CHAR/) CHARO J M.
 PA (OTEN/) OTENHOFF T H M.
 PA (GELU/) GELUK A.
 XX
 PI Kieselring R, Charo JM, Otenhoff TM, Geluk A;
 PI
 DR WPI; 2001-244396/25.
 XX
 DR Novel polypeptides containing epitopes derived from Mycobacterial heat
 PT shock protein 65 useful for treating bacterial and parasitic
 PT infections, such as tuberculosis -
 XX
 XX
 PS Disclosure; Page 55; 117pp; English.
 XX
 XX The present sequence is a peptide epitope derived from Mycobacterial heat
 CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.
 CC Mycobacterium e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
 CC is useful for treating bacterial and parasitic infections such as
 CC tuberculosis.
 CC
 SQ Sequence 9 AA;
 Query Match 43.3%; Score 39; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNV 7
 DB 3 GPKGRNV 7

Db 3 GPKGRNV 9

RESULT 14

ID	AA	94	781	standard; peptide; 15 AA.
xx				

AC AAR94781;

DT 11-NOV-1996 (first entry)

Peptide from library spanning whole of hsp65.

KW Hsp; heat shock protein; *Mycobacterium bovis*; microbial; diagnosis;
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KW prophylaxis.

Synthetic.

PN WO9610039-A1.

PD 04-APR-1996

PF 27-SEP-1995; 95WO-GB02295.
XX

PR 27-SEP-1994; 94GB-0019553.
VY

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Elson CJ, Thompson SJ;
xy

DR WPI; 1996-200888/20.

PT Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g
PT rheumatoid arthritis.

PS Example 1; Figure 1; 88pp; English.

CC
CC
CC ABR94773. R94878 are overlapping peptides of a library spanning the
CC whole of Micaelab hsp65 (heat shock protein 65). Eleven antigens were
CC prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see ABR94772). Peptides concg. this sequence are used in the diagnosis
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.

SQ Sequence 15 AA;

Query Match	Score 38;	DB 17;	Length 15;
42.2%			

Matches	6;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

Qy	11	KKWGAP	16
Db	1	KKWGAP	6

Db 1 KKWGAP 6

RESULT 15
AAW43459

XX

XX

3 XX

Mycobacteria sp. hsp68 derived peptide (group 1 #9).

KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic
 KW pristanе induced arthritis; PIA.

XX Synthetic.
OS Mycobacteria sp.
OS

PN WO9711966-A1.

PD 03-APR-1997

PF 26-SEP-1996; 96WO-GB02382.
VY

PR 27-SEP-1995; 95GB-0019737.
VY

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX

PI Elson CJ, Thompson JS;
YY

WPI; 1997-212851/19.

PT	Polypeptide(s) derived from microbial heat shock protein - useful for treatment of autoimmune disease esp. arthritis
----	--

PS Disclosure; Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAM44351-443556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study
CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAM44351 to AAM44460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAM1948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.

SQ Sequence 15 AA;

Query Match	Score	DB	Length
42.2%	38	18	15

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	11	KKWGAP	16
Db	1	KKWGAP	6

Db 1 KKWGAP 6

Search completed: December 30, 2003, 16:31:43
Job time : 36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:33:07 ; Search time 24.5 Seconds

(without alignments)
129.971 Million cell updates/sec

Title: US-09-847-637b-2

Sequence: 1 GPKGRNVVLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 133148

Minimum DB seq length: 0
Maximum DB seq length: 16Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	10	US-09-847-637b-2
2	55	61.1	16	10	US-09-847-637b-3
3	34	37.8	14	10	US-09-848-664-3
4	34	37.8	14	12	US-10-323-046-12
5	34	37.8	14	12	US-10-405-339-5
6	34	37.8	14	12	US-10-297-329-56
7	34	37.8	14	15	US-10-106-804b-10
8	31	34.4	14	11	US-09-852-455-68
9	30	33.3	14	10	US-09-805-301-80
10	30	33.3	16	12	US-10-161-791-228
11	29.5	32.8	16	15	US-10-225-567A-1359
12	29	32.2	15	10	US-09-976-674-61
13	29	32.2	15	12	US-10-194-441A-16
14	29	32.2	15	12	US-10-194-441A-18
15	28.5	31.7	10	11	US-09-572-404B-1036

16	28	31.1	12	15	US-10-185-050-184	Sequence 184, App
17	28	31.1	15	12	US-10-138-195-16	Sequence 16, Appl
18	27	30.0	8	10	US-09-984-056-58	Sequence 58, Appl
19	27	30.0	8	10	US-09-984-056-59	Sequence 59, Appl
20	27	30.0	8	10	US-09-984-057-58	Sequence 58, Appl
21	27	30.0	8	10	US-09-984-057-59	Sequence 59, Appl
22	27	30.0	8	12	US-10-105-232-58	Sequence 58, Appl
23	27	30.0	8	12	US-10-105-232-59	Sequence 59, Appl
24	27	30.0	8	12	US-10-189-437-58	Sequence 58, Appl
25	27	30.0	8	12	US-10-189-437-59	Sequence 59, Appl
26	27	30.0	14	11	US-09-824-438-20	Sequence 20, Appl
27	27	30.0	14	12	US-10-125-869A-97	Sequence 97, Appl
28	27	30.0	14	12	US-10-125-869A-103	Sequence 103, App
29	26	28.9	8	9	US-09-765-527-237	Sequence 237, App
30	26	28.9	9	9	US-09-732-411-6	Sequence 6, Appl
31	26	28.9	9	15	US-09-866-510-32	Sequence 32, Appl
32	26	28.9	9	15	US-10-091-724-8	Sequence 8, Appl
33	26	28.9	10	12	US-10-237-852-78	Sequence 78, Appl
34	26	28.9	12	12	US-10-119-528-100	Sequence 100, App
35	25.5	28.3	15	12	US-10-283-423-181	Sequence 181, App
36	25.5	28.3	15	12	US-10-213-821-181	Sequence 181, App
37	25	27.8	6	10	US-09-828-272A-7	Sequence 7, Appl
38	25	27.8	6	12	US-10-426-647-7	Sequence 7, Appl
39	25	27.8	6	15	US-10-193-709-15	Sequence 15, Appl
40	25	27.8	6	15	US-10-235-682-7	Sequence 7, Appl
41	25	27.8	7	12	US-10-300-699-46	Sequence 46, Appl
42	25	27.8	7	12	US-10-213-742-10	Sequence 10, Appl
43	25	27.8	8	10	US-09-828-272A-3	Sequence 3, Appl
44	25	27.8	8	12	US-10-426-647-3	Sequence 3, Appl
45	25	27.8	8	12	US-10-297-229-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-847-637b-2
Sequence 2, Application US/09847637b
Patent No. US20020150586A1
GENERAL INFORMATION:
APPLICANT: Naparsky, Yaakov
APPLICANT: Naparsky, Rita
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
FILE REFERENCE: 13125-002001
CURRENT APPLICATION NUMBER: US/09/847,637b
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: PCT/IL99/00595
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,213
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 16
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-847-637b-2

Query Match 100.0%; Score 90; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GPKGRNVVLEKKMGAP 16
Db 1 GPKGRNVVLEKKMGAP 16

RESULT 2
US-09-847-637b-3
Sequence 3, Application US/09847637b

Patent No. US20020150586A1
GENERAL INFORMATION:
APPLICANT: Napatek, Yaakov
APPLICANT: Umaneky, Rina
APPLICANT: Kashi, Yecheskel
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
FILE REFERENCE: 13125-002001
CURRENT APPLICATION NUMBER: US/09/847, 637B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: PCT/IL99/00595
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,213
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 16
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-3

Query Match 61.1%; Score 55; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLEKKMGAP 16
Db 1 VLEKKMGAP 10

RESULT 3
US-09-848-664-3
Sequence 3, Application US/09848664
Patent No. US2002014641A1
GENERAL INFORMATION:
APPLICANT: Sakiyama-Elbert, Shelly E.
APPLICANT: Hubbell, Jeffrey A.
TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth
TITLE OF INVENTION: Factors from Heparin Containing Matrices
FILE REFERENCE: ETH 108
CURRENT APPLICATION NUMBER: US/09/848, 664
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/298,084
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-848-664-3

Query Match 37.8%; Score 34; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11
Db 3 KGRNVLEK 11

RESULT 4
US-10-323-046-12
Sequence 12, Application US/10323046
Publication No. US20030187232A1
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schemse, Jason C.
APPLICANT: Sakiyama-Elbert, Shelly E.
TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue
TITLE OF INVENTION: Engineering

FILE REFERENCE: ETH 107 CIP (2)
CURRENT APPLICATION NUMBER: US/10/323,046
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/141,153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 12
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-10-323-046-12

Query Match 37.8%; Score 34; DB 12; Length 14;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11
Db 3 KGRNVLEK 11

RESULT 5
US-10-405-339-5
Sequence 5, Application US/10405339
Publication No. US20030190364A1
GENERAL INFORMATION:
APPLICANT: Panitch, Alyssa
APPLICANT: Seal, Brandon
TITLE OF INVENTION: Biological Affinity Based Delivery Systems
FILE REFERENCE: 9138-0079US
CURRENT APPLICATION NUMBER: US/10/405,339
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/369,568
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-405-339-5

Query Match 37.8%; Score 34; DB 12; Length 14;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11
Db 3 KGRNVLEK 11

RESULT 6
US-10-297-229-56
Sequence 56, Application US/10297229
Publication No. US20030220245A1
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: SCHOENMAKERS, Ronald
TITLE OF INVENTION: CONTROLLED DELIVERY OF PHARMACEUTICALLY ACTIVE COMPOUNDS
FILE REFERENCE: 50154/003002
CURRENT APPLICATION NUMBER: US/10/297,229
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/US01/18101
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 09/586,937

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:30:27 ; Search time 14 Seconds

(Without alignments)
48.355 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVVLEKMGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 133293

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUTS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	40.0	8	2	US-08-467-822-11
2	36	40.0	8	3	US-08-432-697-11
3	36	40.0	8	3	US-08-466-248-11
4	34	37.8	14	4	US-09-675-922-12
5	30	33.3	9	4	US-09-289-942A-5
6	30	33.3	14	4	US-08-584-043A-80
7	30	33.3	16	3	US-08-602-999A-228
8	30	33.3	16	4	US-09-500-124-228
9	29.5	32.8	15	4	US-09-020-846-38
10	29	32.2	13	5	PCT-US95-07543-3
11	28	31.1	16	1	US-08-300-386A-38
12	28	31.1	16	3	US-08-931-645-38
13	28	31.1	16	5	PCT-US94-01258-38
14	28	31.1	16	5	PCT-US95-11235-38
15	27	30.0	9	1	US-08-452-083-23
16	27	30.0	9	1	US-08-468-557-12
17	27	30.0	10	2	US-08-556-597-158
18	27	30.0	14	4	US-09-217-228-20
19	27	30.0	15	3	US-08-491-954-9
20	26	28.9	6	1	US-08-076-092-56
21	26	28.9	6	2	US-08-730-486-56
22	26	28.9	7	1	US-08-076-092-53
23	26	28.9	7	1	US-08-730-486-53
24	26	28.9	8	1	US-08-076-092-49
25	26	28.9	8	2	US-08-672-610A-48
26	26	28.9	8	2	US-08-621-803-237
27	26	28.9	8	2	US-08-621-259A-239

28	26	28.9	8	2	US-08-621-259A-243	Sequence 243, App
29	26	28.9	8	2	US-08-730-486-49	Sequence 49, Appl
30	26	28.9	8	3	US-09-296-284-14	Sequence 14, Appl
31	26	28.9	8	3	US-09-217-352-237	Sequence 237, Appl
32	26	28.9	9	1	US-08-076-092-42	Sequence 42, Appl
33	26	28.9	9	2	US-08-730-486-42	Sequence 42, Appl
34	26	28.9	9	3	US-09-188-579-109	Sequence 109, App
35	26	28.9	9	3	US-09-315-444-109	Sequence 109, App
36	26	28.9	9	4	US-09-721-362-109	Sequence 109, App
37	26	28.9	10	3	US-08-159-339A-812	Sequence 812, App
38	26	28.9	11	6	5248606-34	Patent No. 5248606
39	26	28.9	12	1	US-07-778-233B-36	Sequence 36, Appl
40	26	28.9	12	1	US-07-963-321-36	Sequence 36, Appl
41	26	28.9	12	1	US-08-290-641-36	Sequence 36, Appl
42	26	28.9	12	1	US-08-330-599-10	Sequence 10, Appl
43	26	28.9	12	1	US-08-548-540-36	Sequence 36, Appl
44	26	28.9	12	2	US-08-726-306A-156	Sequence 156, App
45	26	28.9	12	5	PCT-US96-09809-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-467-822-11
; Sequence 11, Application US/08467822
; Patent No. 5843460
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauterbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thibierge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HERICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467, 822
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,697
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495, 0137-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-822-11

Query Match
Best Local Similarity 40.0%; Score 36; DB 2; Length 8;
85.7%; Pred. No. 2.5e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNV 7
||:||||
Db 2 GPKGRNV 8

RESULT 2
US-08-432-697-11
Sequence 11, Application US/08432697
Patent No. 6248330

GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-432-697-11

Query Match
Best Local Similarity 40.0%; Score 36; DB 3; Length 8;
85.7%; Pred. No. 2.5e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNV 7
||:||||
Db 2 GPKGRNV 8

RESULT 3
US-08-466-248-11
Sequence 11, Application US/08466248

Patent No. 6258359
GENERAL INFORMATION:

APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-248-11

Query Match
Best Local Similarity 40.0%; Score 36; DB 3; Length 8;
85.7%; Pred. No. 2.5e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNV 7
||:||||
Db 2 GPKGRNV 8

RESULT 4
US-09-675-922-12
Sequence 12, Application US/09675922
Patent No. 6468731

GENERAL INFORMATION:
APPLICANT: Hubbell A., Jeffrey
APPLICANT: Schense C., Jason
APPLICANT: Sakiyama E., Shelley
TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue
FILE REFERENCE: ETH 107 DIV
CURRENT APPLICATION NUMBER: US/09/675,922

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:29:06 ; Search time 13.5 Seconds
(without alignments)
113.978 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKMGAPITTDG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 2770

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	29.9	15	2	PH1631
2	25	28.7	13	1	MTCMAD
3	25	28.7	13	1	MTMHAD
4	24	27.6	14	2	154945
5	22	25.3	8	2	A31570
6	22	25.3	13	2	G83988
7	21	24.1	11	2	S09074
8	21	24.1	13	2	A32734
9	21	24.1	13	2	A86126
10	21	24.1	14	2	S03530
11	21	24.1	15	2	S10388
12	21	24.1	16	2	PS0383
13	21	24.1	16	2	S26746
14	21	24.1	16	2	E28027
15	21	24.1	16	2	I37452
16	20	23.0	10	2	S42282
17	20	23.0	13	2	S47371
18	20	23.0	13	2	PH0928
19	20	23.0	13	4	I70076
20	20	23.0	14	2	S13864
21	20	23.0	14	2	A59018
22	20	23.0	15	2	S26791
23	20	23.0	15	2	S29386
24	20	23.0	15	2	T46625
25	20	23.0	15	2	A56970
26	20	23.0	15	2	S10386
27	20	23.0	16	1	MTDFBS
28	20	23.0	16	2	S03532
29	20	23.0	16	2	D49021

ALIGNMENTS

30	20	23.0	16	2	PH0749	T-cell receptor be
31	19	21.8	9	2	B38740	Ig kappa chain C r
32	19	21.8	10	1	XAV168	angiotensin-conver
33	19	21.8	10	2	PH1344	Ig heavy chain DJ
34	19	21.8	10	2	F33932	Ig mu chain J regi
35	19	21.8	11	2	PH1343	Ig heavy chain DJ
36	19	21.8	12	2	PH1324	Ig heavy chain DJ
37	19	21.8	13	2	S04014	lignin peroxidase
38	19	21.8	13	2	S57567	T cell receptor V-
39	19	21.8	13	2	A32486	beta protein - rat
40	19	21.8	13	2	I51905	collecting duct wa
41	19	21.8	14	2	PS0249	porin - rice (stra
42	19	21.8	14	2	PT0223	Ig heavy chain CDR
43	19	21.8	14	2	PH1356	Ig heavy chain DJ
44	19	21.8	14	2	PH1332	Ig heavy chain DJ
45	19	21.8	15	2	S21241	oligo-1,6-glucosid

RESULT 1

PH1631
Ig H chain V-D-J region (clone B-less 202) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1631
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1631
A/Molecule type: DNA
A/Residues: 1-15 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match

Best Local Similarity 29.9%; Score 26; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PTITNDG 16
DB 4 PMVTTDG 10

RESULT 2

MTCMAD
melanotropin alpha - Arabian camel
C/Species: Camelus dromedarius (Arabian camel)
C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998
C/Accession: A01464
R/Li, C.H.; Danho, W.O.; Chung, D.; Rao, A.J.
Biochemistry 14, 947-952, 1975
A>Title: Isolation, characterization, and amino acid sequence of melanotropins from cam
A/Reference number: A90393; MUID:75146434; PMID:1125179
A/Accession: A01464
A/Molecule type: protein
A/Residues: 1-13 <LIC>
C/Superfamily: corticotropin-lipotropin
C/Keywords: acetylated amino end; blocked carboxyl end; hormone; pituitary
F.1/Modified site: acetylated amino end (Ser) (partial) #status experimental
F.13/Modified site: blocked carboxyl end (Val) (probably undated) #status experimental

Query Match

Best Local Similarity 28.7%; Score 25; DB 1; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 RWGAP 10
DB 8 RWGAP 12

RESULT 3

MTHOAD

melanotropin alpha - horse

C/Species: Equus caballus (domestic horse)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998

C/Accession: A91785; A01464

R/Dixon, J.S.; Li, C.H.

J. Am. Chem. Soc. 82, 4568-4572, 1960

A/Title: The isolation and structure of alpha-melanocyte-stimulating hormone from horse

A/Reference number: A91785

A/Accession: A91785

A/Molecule type: protein

A/Residues: 1-13 <DX>

C/Superfamily: corticotropin-lipotropin

C/Keywords: blocked amino end; blocked carboxyl end; hormone; pituitary

F1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental

F13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match

Best Local Similarity 28.7%; Score 25; DB 1; Length 13;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KMGAP 10

DB 8 RMGKP 12

RESULT 4

154945

gene C protein - Escherichia coli (fragment)

C/Species: Escherichia coli

C/Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999

C/Accession: 154945

R/Tao, T.; Bourne, J.C.; Blumenthal, R.M.

J. Bacteriol. 173, 1367-1375, 1991

A/Title: A family of regulatory genes associated with type II restriction-modification

A/Reference number: 154945; PMID:91139577; PMID:1995588

A/Accession: 154945

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-14 <RBS>

A/Cross-references: GB:M63619; NID:g147664; PIDN:AAA24555.1; PID:g147665

Query Match

Best Local Similarity 27.6%; Score 24; DB 2; Length 14;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKK 6

DB 4 VIMEKK 9

RESULT 5

A31570

angiotensin-converting enzyme inhibitor - yellowfin tuna

C/Species: Thunnus albacares (yellowfin tuna)

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000

C/Accession: A31570

R/Kohama, Y.; Matsunoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.

Biochem. Biophys. Res. Commun. 155, 332-337, 1988

A/Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.

A/Reference number: A31570; MUID:88326322; PMID:3415688

A/Accession: A31570

A/Molecule type: protein

A/Residues: 1-8 <KOH>

A/Note: the source is designated as Neothunnus macropterus

C/Superfamily: unassigned animal peptides

C/Keywords: angiotensin-converting enzyme inhibitor

Query Match

Best Local Similarity 25.3%; Score 22; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KMG 8

DB 5 KMG 7

RESULT 6

G83988

hypothetical protein BH2711 (imported) - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C/Accession: G83988

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hix

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: G83988

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-13 <STO>

A/Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06430.1; GSPDB:GNC

A/Experimental source: strain C-125

C/Genetics:

A/Gene: BH2711

Query Match

Best Local Similarity 25.3%; Score 22; DB 2; Length 13;

Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 VLEKMGAPTI 12

DB 1 MIOGRFSKPMI 11

RESULT 7

S09074

cytochrome P450-4b - rat (fragment)

N/Alternate names: cytochrome P450K-5

N/Contains: oxidoreductase (EC 1.-.-.-)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999

C/Accession: S09074

R/Imaoka, S.; Terano, Y.; Runae, Y.

Arch. Biochem. Biophys. 278, 168-178, 1990

A/Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with star

A/Reference number: S09074; MUID:90210577; PMID:2321956

A/Accession: S09074

A/Molecule type: protein

A/Residues: 1-11 <IMA>

C/Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C/Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match

Best Local Similarity 24.1%; Score 21; DB 2; Length 11;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PTTINDG 16

DB 4 PTXSLDG 10

RESULT 8

A32734

enkephalin precursor - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000

C/Accession: A32734

R/Micanovic, R.; Ray, P.; Krugel, W.; Lewis, R.V.

Biochem. Biophys. Res. Commun. 118, 299-303, 1984

A/Title: Purification and sequence of an opioid peptide derived from ovine proenkephal:

A/Reference number: A32734; MUID:84128045; PMID:6546517

A/Accession: A32734

A/Status: preliminary

A/Molecule type: protein

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:26:11 ; Search time 10 Seconds
(without alignments)
75.243 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKWGAPITNDG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 872

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.7	13	1	MIA_ANOCA
2	25	28.7	13	1	MIA_CAMDR
3	25	28.7	13	1	UNOI_PINS
4	23	26.4	11	1	ASL2_BACSE
5	22	25.3	8	1	ACI_THUAL
6	22	25.3	10	1	UNAJ_HUMAN
7	20	23.0	13	1	UNOJ_PINS
8	20	23.0	14	1	MCRX_METM
9	20	23.0	16	1	MIB_SQUAC
10	19	21.8	10	1	BPP2_BOTJA
11	19	21.8	12	1	UP01_CABEL
12	19	21.8	13	1	LIGB_TRAVE
13	19	21.8	14	1	SAP2_ABPBU
14	18	20.7	8	1	RT34_BOVIN
15	18	20.7	10	1	BPP2_BOVIN
16	18	20.7	10	1	BPP8_BOVIN
17	18	20.7	10	1	BPP_VIPAS
18	18	20.7	12	1	PEP3_PHYPA
19	18	20.7	13	1	LIGA_TRAVE
20	18	20.7	13	1	PBBP_PINS
21	18	20.7	15	1	TY13_PHYRO
22	18	20.7	15	1	MAL7_BACTO
23	17.5	20.1	5	1	BPP7_BOVIN
24	17	19.5	6	1	CBP2_MYTED
25	17	19.5	6	1	LOK1_LOCHI
26	17	19.5	8	1	LCK1_LEUMA
27	17	19.5	8	1	LCK2_LEUMA
28	17	19.5	8	1	LCK3_LEUMA
29	17	19.5	8	1	LCK4_LEUMA
30	17	19.5	8	1	LCK5_LEUMA
31	17	19.5	8	1	LCK6_LEUMA
32	17	19.5	8	1	LCK7_LEUMA
33	17	19.5	8	1	LCK8_LEUMA

34	17	19.5	9	1	PAR5_ASCSU	P43170	ascaris	smu
35	17	19.5	10	1	PAR6_PANRE	P82660	panagrellus	
36	17	19.5	10	1	HTF1_ROMMI	P18110	romalea	mic
37	17	19.5	10	1	HTF2_CARMO	P13385	carausius	m
38	17	19.5	10	1	HTF_HILZE	P16353	heliothis	z
39	17	19.5	10	1	HTF_NAUCI	P10939	nauphoeta	c
40	17	19.5	10	1	HTF_TABAT	P14596	tabanus	atr
41	17	19.5	10	1	LABA_JATMU	P13270	jatropha	mu
42	17	19.5	10	1	LPK2_LOCHI	P41488	locusta	mig
43	17	19.5	10	1	UPA9_HUMAN	P30095	homo	sapien
44	17	19.5	12	1	H2AX_ONCMY	P83327	oncorhynch	
45	17	19.5	13	1	IDHP_RAT	P56574	rattus	norv

ALIGNMENTS

RESULT 1
MIA_ANOCA STANDARD; PRT; 13 AA.
AC P41589;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
DS Melanotropin alpha (Alpha-MSH). (American chameleon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosteura; Squamata; Iguania; Polychrotinae; Anolis.
OX NCBI_TaxID=28377;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary; PubMed=1667689;
RX MEDLINE=92270473; PubMed=1667689;
RA Doses R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;
RT Isolation of a novel sequence change in the major form of alpha-MSH
RT isolated from the intermediate pituitary of the reptile, Anolis
RT carolinensis. "
RL Peptides 12:1261-1266(1991).
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR InterPro: IPR001941; Mcoitin ACTH.
DR Pfam: PF00976; ACTH_domain; I.
KM Hormone; Amidation.
FT MOD RES 13
FT MOD RES 13
SQ SEQUENCE 13 AA; 1608 MW; FF990A7358BB09C1 CRC64;

Query Match 28.7%; Score 25; DB 1; Length 13;
Best local similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 6 RWGAP 10
DB 8 RWGAP 12

RESULT 2

MIA_CAMDR STANDARD; PRT; 13 AA.
AC P01198;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
DS Camelus dromedarius (Dromedary) (Arabian camel), and
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838, 9796;
RN [1]
RP SEQUENCE.
RC SPECIES=C. dromedarius;
RX MEDLINE=75146434; PubMed=1125179;
RA Li C.H., Danto W.O., Chung D., Rao A.J.;
RT Isolation, characterization, and amino acid sequence of

RESULT 4			
ASL2_BACSE	STANDARD;	PRT;	11 AA.
AC P83147;			
DT 28-FEB-2003 (Rel. 41, Created)			
DT 28-FEB-2003 (Rel. 41, Last sequence update)			
DT 28-FEB-2003 (Rel. 41, Last annotation update)			
DE Acharan sulfatase 2 (EC 4.2.2.-) (fragment).			
OS Bacteroides stercoris.			
OC Bacterioidetes; Bacteroidales; Bacteroides (class); Bacteroidales; Bacteroidaceae; Bacteroides.			
OX NCBI_TaxID=46506;			
RN [1]			
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.			
RC STRAIN=HJ-15;			
RX MEDLINE=21223019; PubMed=11322884;			
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;			
"Purification and characterization of acharan sulfatase 2 from Bacteroides stercoris HJ-15."			
RT Eur. J. Biochem. 268:2635-2641(2001).			
CC -1- FUNCTION: Degrades acharan sulfate and, to a lesser extent, heparin and heparan sulfate.			
CC -1- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.			
CC Activated by reducing agents, such as DL-dithiothreitol and 2-mercaptoethanol.			
CC -1- SUBUNIT: Monomer.			
CC -1- PTM: The N-terminus is blocked.			
CC -1- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is 7.2 and optimum temperature 45 degrees Celsius.			
KW Lyase; Heparin-binding.			
FT NON TER	1		
FT NON TER	1		
SQ SEQUENCE	11 AA; 1195 MW; D79D897C7AA451AD CRC64;		
QY	13 TNDG 16	26.4%; Score 23; DB 1; Length 11;	
DB	5 TNDG 8	Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;	
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RESULT 5			
ACI THVAL	STANDARD;	PRT;	8 AA.
AC P18691;			
DT 01-NOV-1990 (Rel. 16, Created)			
DT 01-NOV-1990 (Rel. 16, Last sequence update)			
DT 01-NOV-1990 (Rel. 16, Last annotation update)			
DE Angiotensin-converting enzyme inhibitor.			
OS Thunnus albacares (Yellowfin tuna) (Neochannus macropterus).			
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Perciformes; Percutiformes; Scombroidei; Scombridae; Thunnus.			
CC NCBI_TaxID=8236;			
RN [1]			
RP SEQUENCE.			
RC TISSUE=Muscle;			
RX MEDLINE=88326322; PubMed=3415688;			
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;			
"Isolation of angiotensin-converting enzyme inhibitor from tuna muscle."			
RT Blochem. Biophys. Res. Commun. 155:332-337(1988).			
DR PIR, A31570; A31570.			
SQ SEQUENCE	8 AA; 953 MW; 6AA863733051P1B7 CRC64;		
Query Match	25.3%; Score 22; DB 1; Length 8;		
Best Local Similarity 100.0%; Pred. No. 1.3e+05;			
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:29:41 ; Search time 28 Seconds

(without alignments)
147.459 Million cell updates/sec

Title: US-09-847-637B-3

Sequence: 1 VVLEKMGAPRTTNDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4022

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.7	10	11	070580 mus musculu
2	25	28.7	16	11	045530 O45530 bacillus su
3	25	28.7	16	4	09UCR9 O9UCR9 homo sapien
4	24	27.6	14	2	047599 O47599 escherichia
5	23	26.4	11	15	083410 O83410 mouse mamma
6	23	26.4	13	15	085645 O85645 mouse mamma
7	23	26.4	16	2	010748 O10748 clostridium
8	23	26.4	16	4	09UCR8 O9UCR8 homo sapien
9	23	26.4	16	10	09S8D6 O9S8D6 triticum ae
10	22	25.3	12	15	098240 O98240 human immun
11	22	25.3	13	16	09K9D7 O9K9D7 bacillus ha
12	22	25.3	15	8	099386 O99386 sus scrofa
13	21	24.1	8	8	094PX5 O94PX5 felis silve
14	21	24.1	8	8	094VB2 O94VB2 varanus sal
15	21	24.1	8	8	094PX7 O94PX7 felis silve
16	21	24.1	8	8	094PX6 O94PX6 felis libyc

17	21	24.1	8	8	094VA7 O94VA7 varanus sal
18	21	24.1	8	8	094VB5 O94VB5 varanus sal
19	21	24.1	8	9	08SB0 O8SB0 bacterioph
20	21	24.1	8	9	08H9K1 O8H9K1 bacterioph
21	21	24.1	9	8	094VC6 O94VC6 varanus pil
22	21	24.1	10	8	094VD5 O94VD5 varanus pil
23	21	24.1	12	13	08AUP8 O8AUP8 salmo trut
24	21	24.1	13	8	09MQX0 O9MQX0 cervus elap
25	21	24.1	13	8	09MQK6 O9MQK6 rupicapra r
26	21	24.1	13	8	09MQK3 O9MQK3 capra ibex
27	21	24.1	13	16	08XAF5 O8XAF5 escherichia
28	21	24.1	14	12	P91578 P91578 choristronu
29	21	24.1	15	4	09BXK4 O9BXK4 homo sapien
30	21	24.1	15	8	P92076 P92076 euhadra her
31	21	24.1	16	4	014495 O14495 homo sapien
32	21	24.1	16	5	09NFJ0 O9NFJ0 trypanosoma
33	20	23.0	11	2	09EUZ3 O9EUZ3 escherichia
34	20	23.0	11	15	08ADI8 O8ADI8 human immun
35	20	23.0	12	15	08QDY5 O8QDY5 human immun
36	20	23.0	12	15	08Q347 O8Q347 human immun
37	20	23.0	12	15	08QDY4 O8QDY4 human immun
38	20	23.0	12	15	08Q341 O8Q341 human immun
39	20	23.0	12	15	08Q345 O8Q345 human immun
40	20	23.0	12	15	08Q343 O8Q343 human immun
41	20	23.0	12	15	08QDY6 O8QDY6 human immun
42	20	23.0	13	1	050831 O50831 methanococc
43	20	23.0	13	4	014462 O14462 homo sapien
44	20	23.0	15	6	09TS39 O9TS39 gorilla gor
45	20	23.0	15	10	09S914 O9S914 hordeum vul

ALIGNMENTS

RESULT 1

ID 070580 PRELIMINARY: PRT; 10 AA.
AC 070580;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Carbonic anhydrase III (Fragment).
GN CAR3 OR CAR3 OR CAR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sowden J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter of the carbonic anhydrase 3 (CA3) gene."
RT Gene 214:157-165(1999)
DR EMBL, AJ006474; CAA07057.1; -
DR MGD; MGI:88270; Car3.
DR MGD; MGI:1351477; Car3.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 56F7BE71ADC37B13 CRC64;

Query Match 28.7%; Score 25; DB 11; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LEKKWAP 10
DB 1 MAKEWAP 8

RESULT 2
ID 045530 PRELIMINARY: PRT; 16 AA.
AC 045530;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Chloramphenicol acetyltransferase (EC 2.3.1.28) (Fragment).
 GN CAT.
 OS Bacillus subtilis.
 OC Bacterias; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M168; TRANSPOSON=TN9;
 RX MEDLINE=85113144; PubMed=2982142;
 RA Lin C.K., Goldfarb D.S., Doi R.H., Rodriguez R.L.;
 RT "Mutations that affect the translation efficiency of Tn9-derived cat
 gene in Bacillus subtilis."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:173-177 (1985).
 CC -1- FUNCTION: THIS ENZYME IS AN EFFECTOR OF CHLORAMPHENICOL RESISTANCE
 IN BACTERIA.
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + CHLORAMPHENICOL = COA +
 CC -1- SIMILARITY: BELONGS TO THE CHLORAMPHENICOL ACETYLTRANSFERASE
 CC FAMILY.
 DR EMBL; M12657; AAA22291.1; -
 KM Acyltransferase; Antibiotic resistance; Transferase.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1936 MW; B4894C04C5A5409F CRC64;

 QY Query Match 28.7%; Score 25; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 3
 Q9UCK9 PRELIMINARY; PRT; 16 AA.
 AC Q9UCK9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buthera; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93099171; PubMed=1463770;
 RA Baba S., Takahashi T., Kasama T., Shiraawa H.;
 RT "Identification of two novel amyloid A protein subsets coexisting in
 an individual patient of AA-amyloidosis."
 RL Biochim. Biophys. Acta 1180:195-200 (1992).
 CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 COMPLEX (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
 DR InterPro; IPR000096; Serum amyloid_A.
 DR Pfam; PF00277; SAA_proteins; 1.
 KM Acute phase; HDL.
 SQ SEQUENCE 16 AA; 1612 MW; 1CBA4F077C9C8CC1 CRC64;

 QY Query Match 28.7%; Score 25; DB 4; Length 16;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 4
 ID Q47599 PRELIMINARY; PRT; 14 AA.
 AC Q47599;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE C (Fragment).
 GN C.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 NX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 modification systems."
 RL J. Bacteriol. 173:1367-1375 (1991).
 DR EMBL; M63619; AAA24555.1; -
 FT NON TER 1 1
 SQ SEQUENCE 14 AA; 1705 MW; 77B6CA60581A4F3B CRC64;

 QY Query Match 27.6%; Score 24; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 ID Q83410 PRELIMINARY; PRT; 11 AA.
 AC Q83410;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Superantigen (Fragment).
 GN SAg.
 OS Mouse mammary tumor virus.
 OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
 CX NCBI_TaxID=11757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mtv-6;
 RX MEDLINE=95133174; PubMed=7831795;
 RA Cho K., Patrick D.A., Morris D.W.;
 RT "Structure and biological activity of the subgenomic Mtv-6 endogenous
 RT provirus."
 RL Virology 206:395-402 (1995).
 DR EMBL; U37518; AA66863.1; -
 DR InterPro; IPR001213; MMTV_SAg.
 DR Pfam; PF01054; MMTV_SAg; 1.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1401 MW; 5E6B080A7326CD7 CRC64;

 QY Query Match 26.4%; Score 23; DB 15; Length 11;
 Best Local Similarity 60.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 WGAPTTN 14
 Db 7 WAAEVISN 14

RESULT 6
 ID Q85645 PRELIMINARY; PRT; 13 AA.
 AC Q85645;

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OM protein - protein search, using sw model

Run on: December 30, 2003, 16:25:36 ; Search time 35 Seconds
(without alignments)
72.561 Million cell updates/sec

Title: US-09-847-637B-3
Sequence: 1 VLEKMGAPITTDG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 360314

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	16	AA193330	Amino acid sequenc
2	87	100.0	16	AAU99965	Mycobacterium tube
3	81	93.1	16	AAW43458	Mycobacterium sp. h
4	76	87.4	16	AAW43459	Peptide from libra
5	70	80.5	15	AAW43459	Mycobacterium sp. h
6	65	74.7	15	AAW43459	Peptide from libra
7	55	63.2	16	AAU93329	Amino acid sequenc
8	55	63.2	16	AAU99964	Mycobacterium tube
9	48	55.2	15	AAW43459	Peptide from libra

10	48	55.2	15	AAW43457
11	39	44.8	15	AAW26843
12	39	44.8	16	AAW43458
13	35	40.2	16	AAW87908
14	35	40.2	16	AAW10516
15	34	39.1	16	AAW43459
16	32	36.8	12	AAW86064
17	31.5	36.2	16	AAU83423
18	31.5	36.2	16	AAU83424
19	31.5	36.2	16	AAU83425
20	31	35.6	12	AAW90858
21	31	35.6	12	ABG74642
22	31	35.6	15	AAW14808
23	31	35.6	15	AAW34136
24	31	35.6	15	AAW52607
25	31	35.6	15	AAW52656
26	30	34.5	10	AAW32456
27	30	34.5	10	AAW54380
28	30	34.5	12	AAW08829
29	30	34.5	14	AAW38766
30	30	34.5	14	AAW24451
31	30	34.5	15	ABG61615
32	30	34.5	16	AAW37709
33	30	34.5	16	AAW25443
34	29	33.3	7	ABU04516
35	29	33.3	9	AAW45892
36	29	33.3	13	ABB97728
37	29	33.3	13	ABB97729
38	28	32.2	9	AAW56753
39	28	32.2	12	AAW38002
40	28	32.2	13	AAW48084
41	28	32.2	13	AAE34758
42	28	32.2	14	AAW00664
43	28	32.2	14	AAW026122
44	28	32.2	15	AAW37382
45	28	32.2	15	ABG96155

ALIGNMENTS

```

RESULT 1
AAW93330
ID AAW93330 standard; peptide; 16 AA.
XX
AC AAW93330;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of an epitope of heat shock protein 60.
XX
KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
XX inflammatory disorder; arthritis.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200027870-A1.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99WO-IL00595.
XX
PR 05-NOV-1998; 98US-0107213.
XX
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
PI Naparetek Y, Umaneky R, Kaehi Y;
XX
DR WPI, 2000-376486/32.
XX
PT Peptide having a defined sequence is used in vaccines for conferring
PT immunity against autoimmune disease or inflammatory disorders,
PT especially arthritis -

```

Mycobacteria sp. h
Arabidopsis thaliana
Mycobacteria sp. h
Bovine lactoferrin
Lactoferrin derivative
Peptide from libra
Human glucocerebro
Bacterial fructosyl
Bacterial fructosyl
Melanocyte stimula
C. unshiu FUS pept
fcs oncogene prote
Variant human pote
v-fes encoded onco
fcs-encoded oncop
Human secreted pro
Amino acid sequenc
Human scavenger re
Delivery peptide u
Nucleic acid (NA)
Human DPRP-3 pepti
N terminal of haem
Gcb2 N-terminal SH
Molt-4 leukemia c
Human tumor-associ
Human procathepsin
Human procathepsin
A. tumefaciens ant
WW domain binding
Tie-1 binding surz
Streptomyces sp. s
Human protein frag
Fc region binding
Hepatitis C virus
Cysteine-containin

XX Claim 3; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.

XX Sequence 16 AA;

Query Match 100.0%; Score 87; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKKGAPTTNDG 16
 DB 1 VLEKKKGAPTTNDG 16

RESULT 2

ID AAW99965 standard; Peptide; 16 AA.

AC AAW99965;

DT 07-OCT-2002 (first entry)

DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #2.

XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;
 KM autoimmune disease; infectious disease; graft rejection; type I diabetes;
 KM juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
 KM systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
 KM arteriosclerosis.

XX Mycobacterium tuberculosis.

PN WO200248312-A2.

XX 20-JUN-2002.

PD 11-DEC-2001; 2001WO-IL01144.

PF 11-DEC-2000; 2000IL-0140233.

PR (PEPT-) PEPTOR LTD.

PA Elias D, Avron A, Senderowitz H;

PI WPI; 2002-557613/59.

XX New backbone cyclised peptide analog of heat shock protein useful in
 PT the treatment of e.g. autoimmune disease -

PS Claim 5; Page 42; 50pp; English.

XX The invention relates to backbone cyclised peptide analogues or
 CC antagonists of heat shock protein (hsp). The analogues and antagonists
 CC are useful in the treatment of chronic inflammatory disease, autoimmune
 CC disease, infectious disease and graft rejection, and for diagnosing
 CC autoimmune and inflammatory disease including juvenile rheumatoid
 CC arthritis, type I diabetes, multiple sclerosis, systemic lupus
 CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
 CC arteriosclerosis. This sequence represents a backbone cyclised peptide
 CC analogue of a heat shock protein.

XX Sequence 16 AA;

Query Match 100.0%; Score 87; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKKGAPTTNDG 16
 DB 1 VLEKKKGAPTTNDG 16

RESULT 3

ID AAW43458 standard; peptide; 16 AA.

AC AAW43458;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM pristane induced arthritis; PIA.

XX Synthetic.

OS Mycobacteria sp.

PN WO9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

XX WPI; 1997-212851/19.

XX Polypeptide(s) derived from microbial heat shock protein - useful
 PT for treatment of autoimmune disease esp. arthritis

PS Disclosure; Fig 1a; 91pp; English.

XX This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW4948-W14950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.

XX Sequence 16 AA;

Query Match 93.1%; Score 81; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKKGAPTTND 15
 DB 2 VLEKKKGAPTTND 16

RESULT 4

ID AAR94780 standard; peptide; 16 AA.

AC AAR94780;

XX

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DT 11-NOV-1996 (first entry)
XX
XX Peptide from library spanning whole of hsp65.
DE Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KM prophylaxis.
XX
XX Synthetic.
OS
XX WO9610039-A1.
PN
XX
XX 04-APR-1996.
PD
XX
XX 27-SEP-1995; 95WO-GB02295.
PF
XX
XX 27-SEP-1994; 94GB-0019553.
PR
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
PA
XX Elson CJ, Thompson SJ;
PI
XX WPI; 1996-200888/20.
DR
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
PS
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see AAR94772). Peptides concy. This sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.
XX
SQ Sequence 16 AA;
Query Match 87.4%; Score 76; DB 17; Length 16;
Best Local Similarity 93.3%; Pred. No. 3.2e-06;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy 1 VVEKKMGAPTTND 15
DB 2 VVEKKMGAPTTND 16
RESULT 5
AAM43459
ID AAM43459 standard; peptide; 15 AA.
XX
XX AAM43459;
AC
XX
XX 08-APR-1998 (first entry)
DT
XX
XX Mycobacteria sp. hsp68 derived peptide (group 1 #9).
DE
XX
XX Heat shock protein; hsp68; autoimmune disease; hsp65; vaccine;
KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX pristane induced arthritis; PIA.
XX
XX Synthetic.
OS
XX Mycobacteria sp.
XX
XX WO9711966-A1.
PN
XX
XX 03-APR-1997.
PD
XX
XX 26-SEP-1996; 96WO-GB02382.
PF

```

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XX
XX 27-SEP-1995; 95GB-0019737.
RR
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
PA
XX
XX Elson CJ, Thompson SJ;
PI
XX
XX WPI; 1997-212851/19.
DR
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
PT for treatment of autoimmune disease esp. arthritis
PT
XX
XX Disclosure; Fig 1a; 91pp; English.
PS
XX
XX This peptide is one of a library (see AAM43451-W43556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study
CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAM14948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.
XX
XX Sequence 15 AA;
SQ
Query Match 80.5%; Score 70; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 5 KKGAPTTNDG 16
DB 1 KKGAPTTNDG 12
RESULT 6
AAR94781
ID AAR94781 standard; peptide; 15 AA.
XX
XX AAR94781;
AC
XX
XX 11-NOV-1996 (first entry)
DT
XX
XX Peptide from library spanning whole of hsp65.
DE
XX
XX Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
XX Synthetic.
OS
XX
XX WO9610039-A1.
PN
XX
XX 04-APR-1996.
PD
XX
XX 27-SEP-1995; 95WO-GB02295.
PF
XX
XX 27-SEP-1994; 94GB-0019553.
PR
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
PA
XX Elson CJ, Thompson SJ;
PI
XX
XX WPI; 1996-200888/20.
DR
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX

```

PS Example 1; Figure 1; 88pp; English.

CC AAR94773-R94878 are overlapping peptides of a library spanning the
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.

XX Sequence 15 AA;

Query Match 74.7%; Score 65; DB 17; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00023;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KKWGAPTTNDG 16
DB 1 KKWGAPTTNDG 12

RESULT 7

AAY93329 standard; peptide; 16 AA.

XX AAY93329;

DT 04-SEP-2000 (first entry)

XX Amino acid sequence of an epitope of heat shock protein 60.

KM Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
inflammatory disorder; arthritis.

XX Mycobacterium tuberculosis.

PN WO200027870-A1.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-1100595.

XX 05-NOV-1998; 98US-0107213.

PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.

PI Naparstek Y, Ulimansky R, Kashi Y;

DR WPI; 2000-376486/32.

PT Peptide having a defined sequence is used in vaccines for conferring
PT immunity against autoimmune disease or inflammatory disorders,
PT especially arthritis -

PS Claim 2; Page 7; 58pp; English.

CC The present sequence represents an epitope of the heat shock protein
CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
CC nucleic acid encoding it, are useful in vaccines for conferring
CC immunity against autoimmune disease or inflammatory disorders,
CC especially arthritis. The peptide may also be used to raise
CC antibodies, which are then used for passive immunisation.

XX Sequence 16 AA;

Query Match 63.2%; Score 55; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKWGAP 10
|||

DB 7 VLEKKWGAP 16

RESULT 8
AAU99964 standard; Peptide; 16 AA.

XX AAU99964;

DT 07-OCT-2002 (first entry)

DE Mycobacterium tuberculosis hsp60 backbone cyclised peptide analogue #1.

XX Heat shock protein; hsp; hsp60; chronic inflammatory disease;
XX autoimmune disease; infectious disease; graft rejection; type I diabetes;
XX juvenile rheumatoid arthritis; multiple sclerosis; uveitis; cyclic;
XX systemic lupus erythematosus; inflammatory bowel disease; thyroiditis.
XX arteriosclerosis.

OS Mycobacterium tuberculosis.

PN WO200248312-A2.

PD 20-JUN-2002.

XX 11-DEC-2001; 2001WO-1101144.

XX 11-DEC-2000; 2000IL-0140233.

PA (PEPT-) PEPTOR LTD.

PI Elias D, Avron A, Senderowitz H;

DR WPI; 2002-557613/59.

PT New backbone cyclized peptide analog of heat shock protein useful in
PT the treatment of e.g. autoimmune disease -

XX Claim 5; Page 42; 50pp; English.

CC The invention relates to backbone cyclised peptide analogues or
CC antagonists of heat shock protein (hsp). The analogues and antagonists
CC are useful in the treatment of chronic inflammatory disease, autoimmune
CC disease, infectious disease and graft rejection, and for diagnosing
CC autoimmune and inflammatory disease including juvenile rheumatoid
CC arthritis, type I diabetes, multiple sclerosis, systemic lupus
CC erythematosus, inflammatory bowel disease, uveitis, thyroiditis and
CC arteriosclerosis. This sequence represents a backbone cyclised peptide
CC analogue of a heat shock protein.

XX Sequence 16 AA;

Query Match 63.2%; Score 55; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKWGAP 10
DB 7 VLEKKWGAP 16
|||

RESULT 9

AAR94779 standard; peptide; 15 AA.

XX AAR94779;

DT 11-NOV-1996 (first entry)

DE Peptide from library spanning whole of hsp65.

KM Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;

KM prophylaxis.
 XX
 OS Synthetic.
 XX
 PN WO9610039-A1.
 XX
 PD 04-APR-1996.
 XX
 PF 27-SEP-1995; 95WO-GB02295.
 XX
 PR 27-SEP-1994; 94GB-0019553.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Elson CJ, Thompson SJ;
 DR WPI, 1996-200888/20.
 XX
 PT Polypeptide derived from bacterial heat shock protein 65 - for use
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 PT rheumatoid arthritis.
 XX
 PS Example 1; Figure 1; 88pp; English.
 XX
 CC AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 55.2%; Score 48; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEKKWGA 9
 Db 7 VLEKKWGA 15
 XX
 RESULT 10
 AAW43457
 ID AAW43457 standard; peptide; 15 AA.
 XX
 AC AAW43457;
 XX
 DT 08-APR-1998 (first entry)
 XX
 DE Mycobacteria sp. hsp68 derived peptide (group 1 #7).
 XX
 KM Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM pristane induced arthritis; PIA.
 XX
 OS Synthetic.
 OS Mycobacteria sp.
 XX
 PN WO9711966-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-GB02382.
 XX
 PR 27-SEP-1995; 95GB-0019737.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
 XX
 PI Elson CJ, Thompson JS;
 XX

XX
 DR WPI, 1997-212851/19.
 XX
 PT Polypeptide(s) derived from microbial heat shock protein - useful
 PT for treatment of autoimmune disease esp. arthritis
 XX
 PS Disclosure; Fig 1a; 91pp; English.
 XX
 CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW1948-W1950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 55.2%; Score 48; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEKKWGA 9
 Db 7 VLEKKWGA 15
 XX
 RESULT 11
 AAE26843
 ID AAE26843 standard; peptide; 15 AA.
 XX
 AC AAE26843;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Anabaena variabilis peptide #16 having tocopherol cyclase activity.
 XX
 KM Tocopherol cyclase; 2, 3-dimethylphytylquinol cyclase; tocol; tocopherol;
 KM tocotrienol; food; feed; vitamin E; enzyme.
 XX
 OS Anabaena variabilis.
 XX
 PN WO200263016-A1.
 XX
 PD 15-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-EP00973.
 XX
 PR 02-FEB-2001; 2001EP-0102397.
 XX
 PA (HOPE) ROCHE VITAMINS AG.
 XX
 PI Chougnat A, Friedlein AM, Woggon W;
 DR WPI, 2002-666954/71.
 XX
 PT Novel tocopherol cyclase protein, useful for the biotechnological
 PT production of vitamin E for use in producing food or feed compositions
 PT -
 XX
 PS Example 4; Page 31; 61pp; English.
 XX
 CC The present invention relates to novel tocopherol cyclase (2, 3-dimethyl-
 CC phytylquinol cyclase) proteins and their corresponding polynucleotides.
 CC Tocopherol cyclase proteins catalyse the reaction of 2, 3-dimethyl-5-
 CC phytyl-1,4-benzoquinol to RRR-gamma-tocopherol. They are involved in the
 CC biosynthetic production of tocols, tocopherols or tocotrienols. They are

CC also useful for the production of a food or feed composition comprising
 CC vitamin E. The present sequence is Anabaena variabilis peptide having
 CC tocopherol cyclase activity.

CC Sequence 15 AA;

Query Match 4.8%; Score 39; DB 23; Length 15;
 Best Local Similarity 70.0%; Pred. No. 7.2;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 WCAPITINDG 16
 :|||||
 1 FGAPQIVNDG 10

RESULT 12

AAW43460
 ID AAW43460 standard; peptide; 16 AA.

AC AAW43460;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #10).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KW rheumatoid arthritis; antigen; infectious disease; propylactic;
 KW pristanic induced arthritis; PIA.

XX Synthetic.
 OS Mycobacteria sp.

PN WC9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

DR WPI; 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis

PS Disclosure; Fig 1a; 91p; English.

CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristanic induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW14948-W14950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.

CC Sequence 16 AA;

Query Match 4.8%; Score 39; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PTTINDG 16
 |||||||

DB 1 PTTINDG 7

RESULT 13

AA87908
 ID AAR87908 standard; peptide; 16 AA.

AC AAR87908;

DT 01-MAR-1996 (first entry)

DE Bovine lactoferrin (24-39).

XX antiviral; lactoferrin;

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /note= "optionally this site is acetylated or
 preceded by a peptide"

FT Modified-site 16 /note= "optionally this site may be in amide form
 or followed by a peptide"

FT JF07069915-A.

PN 14-MAR-1995.

PD 02-SEP-1993; 93JP-0240284.

PR 02-SEP-1993; 93JP-0240284.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

DR WPI; 1995-144726/19.

XX Inhibitor against viral infection and proliferation - contains
 peptide having sequence from lactoferrin

XX Claim 4; Page 2; 10pp; Japanese.

XX The sequence is one of six peptides disclosed as having inhibitory
 CC effect against viral infection. The peptides are derived from
 CC lactoferrin. Their activity is demonstrated against cytomegalovirus.

XX Sequence 16 AA;

Query Match 40.2%; Score 35; DB 16; Length 16;
 Best Local Similarity 77.8%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 KKWGAPRIT 13
 |||||||

DB 4 KQCAPSIT 12

RESULT 14

AAW10516
 ID AAW10516 standard; peptide; 16 AA.

AC AAW10516;

DT 02-APR-1997 (first entry)

DE Lactoferrin derived antibacterial peptide.

XX Lactoferrin; antibacterial; immunogen; monoclonal; antibody;

XX human; bovine; hybridoma; sensitive; specific; detection;

XX determination; gastric juice; intestine; faeces; blood; urine.

XX Synthetic.

```

PN JP0826099-A.
XX
PD 15-OCT-1996.
XX
PF 30-MAR-1995; 95JP-00731177.
XX
PR 30-MAR-1995; 95JP-00731177.
XX
PA (MORG ) MORINAGA MILK IND CO LTD.
XX
DR WPI; 1996-515017/51.
XX
PT Monoclonal antibody combined with bovine or non-natural human
PT lactoferrin fragment - for detecting lactoferrin-originated
PT antibacterial peptide in e.g. gastric juice, urine etc
XX
PS Claim 3; Page 12; 13pp; Japanese.
XX
CC The present peptide is a lactoferrin (LF) derived antibacterial
CC peptide, which can be used as an immunogen in the prepn. of a
CC monoclonal antibody (Mab), capable of binding with a human or
CC bovine LF fragment but not with natural LF, using standard
CC hybridoma techniques. The Mab can be used for the highly sensitive
CC and specific detection or determination of LF derived antibacterial
CC peptides in gastric juice, intestinal contents, faeces, blood and
CC urine.
XX
SQ Sequence 16 AA;

Query Match 40.2%; Score 35; DB 17; Length 16;
Best Local Similarity 77.8%; Pred. NO. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KKWGAPRTT 13
DB 2 KKGAPPSIT 10

RESULT 15
AAR94782
ID AAR94782 standard; peptide; 16 AA.
XX
AC AAR94782;
XX
DT 11-NOV-1996 (first entry)
XX
DE Peptide from library spanning whole of hsp65.
XX
KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KW prophylaxis.
XX
OS Synthetic.
XX
PN WO9610039-A1.
XX
PD 04-APR-1996.
XX
PF 27-SEP-1995; 95WO-GB02295.
XX
PR 27-SEP-1994; 94GB-0019553.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Bison CJ, Thompson SJ;
XX
DR WPI; 1996-200888/20.
XX
PT Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX
PS Example 1; Figure 1; 86pp; English.

```

```

XX
CC AAR94773-R94878 are overlapping peptides of a library spanning the
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.
XX
SQ Sequence 16 AA;

Query Match 39.1%; Score 34; DB 17; Length 16;
Best Local Similarity 85.7%; Pred. NO. 57;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 PTINDG 16
DB 1 PTINDG 7

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Search completed: December 30, 2003, 16:31:43
Job time : 35 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:33:07 ; Search time 24.5 Seconds
(without alignments)
129.971 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87
Sequence: 1 VVLEKKMGAPITNDG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 133148

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	55	63.2	16	10	US-09-847-637B-2 Sequence 2, Appl1
3	32	36.8	9	12	US-10-228-1-67A-3 Sequence 3, Appl1
4	32	36.8	12	10	US-09-753-126-100 Sequence 100, Appl
5	32	36.8	12	11	US-09-896-896A-64 Sequence 64, Appl
6	31.5	36.2	16	10	US-09-995-587A-33 Sequence 33, Appl
7	31.5	36.2	16	10	US-09-995-587A-34 Sequence 34, Appl
8	31.5	36.2	16	10	US-09-995-587A-35 Sequence 35, Appl
9	31.5	36.2	16	10	US-09-995-587A-36 Sequence 36, Appl
10	31	35.6	15	12	US-10-350-405-5 Sequence 5, Appl1
11	31	35.6	15	12	US-10-350-405-217 Sequence 217, Appl
12	31	35.6	15	15	US-10-121-746-70 Sequence 70, Appl
13	30	34.5	14	10	US-09-805-301-80 Sequence 80, Appl
14	30	34.5	15	10	US-09-976-674-61 Sequence 61, Appl
15	30	34.5	16	12	US-10-161-791-228 Sequence 228, Appl

16	29	33.3	13	12	US-10-230-033-40	Sequence 40, Appl
17	28	32.2	12	15	US-10-185-050-184	Sequence 184, Appl
18	28	32.2	13	11	US-09-852-455-68	Sequence 68, Appl
19	28	32.2	13	15	US-10-145-415-65	Sequence 65, Appl
20	28	32.2	13	15	US-10-057-789-227	Sequence 227, Appl
21	28	32.2	13	15	US-10-212-628-227	Sequence 227, Appl
22	28	32.2	14	12	US-10-125-669A-102	Sequence 102, Appl
23	27	31.0	14	11	US-09-824-438-20	Sequence 20, Appl
24	27	31.0	14	12	US-10-195-730-253	Sequence 253, Appl
25	27	31.0	14	12	US-10-125-669A-97	Sequence 97, Appl
26	27	31.0	15	12	US-10-125-669A-103	Sequence 103, Appl
27	27	31.0	15	12	US-10-138-195-16	Sequence 16, Appl
28	26	29.9	8	9	US-09-765-527-237	Sequence 237, Appl
29	26	29.9	9	9	US-09-732-411-6	Sequence 6, Appl1
30	26	29.9	9	10	US-09-866-510-32	Sequence 32, Appl
31	26	29.9	9	15	US-10-091-724-8	Sequence 8, Appl1
32	26	29.9	10	12	US-10-237-852-78	Sequence 78, Appl
33	26	29.9	14	8	US-08-424-550B-455	Sequence 455, Appl
34	26	29.9	14	11	US-09-906-393A-3	Sequence 3, Appl1
35	26	29.9	15	15	US-10-225-567A-1448	Sequence 1448, Appl
36	26	29.9	16	9	US-09-844-813-11	Sequence 11, Appl
37	26	29.9	16	12	US-10-031-874A-164	Sequence 164, Appl
38	25	28.7	6	10	US-09-828-272A-7	Sequence 7, Appl1
39	25	28.7	6	12	US-10-426-647-7	Sequence 7, Appl1
40	25	28.7	6	15	US-10-193-709-15	Sequence 15, Appl1
41	25	28.7	6	15	US-10-235-682-7	Sequence 7, Appl1
42	25	28.7	7	12	US-10-300-699-46	Sequence 46, Appl1
43	25	28.7	7	12	US-10-213-742-10	Sequence 10, Appl1
44	25	28.7	8	10	US-09-828-272A-3	Sequence 3, Appl1
45	25	28.7	8	12	US-10-426-647-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-847-637B-3
Sequence 3, Application US/09847637B
Patent No. US20020150586A1
GENERAL INFORMATION:
APPLICANT: Naparstek, Yaakov
APPLICANT: Ulmaneky, Rita
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
FILE REFERENCE: 13125-002001
CURRENT APPLICATION NUMBER: US/09/847, 637B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: PCT/IL99/00595
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107, 213
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 16
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-3
Query Match 100.0%; Score 87; DB 10; Length 16;
Best local similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VVLEKKMGAPITNDG 16
1 VVLEKKMGAPITNDG 16
RESULT 2
US-09-847-637B-2
Sequence 2, Application US/09847637B

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Patent No. US20020150586A1
GENERAL INFORMATION:
APPLICANT: Napatstek, Yaakov
APPLICANT: Ulanetsky, Rina
APPLICANT: Kashi, Yechezkel
TITLE OF INVENTION: NOVEL AMINO ACID SEQUENCES, DNA ENCODING
TITLE OF INVENTION: THE AMINO ACID SEQUENCES, ANTIBODIES DIRECTED AGAINST SUCH
TITLE OF INVENTION: SEQUENCES AND THE DIFFERENT USES THEREOF
FILE REFERENCE: 13125-002001
CURRENT APPLICATION NUMBER: US/09/847,637B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: PCT/IL99/00595
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,213
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 16
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-847-637B-2

Query Match      63.2%; Score 55; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAP 10
Db 7 VLEKKMGAP 16

RESULT 3
US-10-228-167A-3
Sequence 3, Application US/10228167A
Publication No. US20030147909A1
GENERAL INFORMATION:
APPLICANT: Hernan Marshall Gonzalez, Sergio
TITLE OF INVENTION: HIGHLY IMMUNOGENIC PROTEIN AGAINST THE INTRACELLULAR PATHOGEN AG
TITLE OF INVENTION: PISCIRICKETTSIA SALMONIS, WHICH AFFECTS SALMON CULTURE, AMINO AC
TITLE OF INVENTION: ACID SEQUENCES OF SAID PROTEIN AND ITS APPLICATION IN THE DEVELO
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND DIAGNOSIS OF DISEASES CAUSED BY S
FILE REFERENCE: 076502-9004
CURRENT APPLICATION NUMBER: US/10/228,167A
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: Chilean Patent Application No. US20030147909A1 2086-2001
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 9
TYPE: PRT
ORGANISM: Piscirickettsia salmonis
US-10-228-167A-3

Query Match      36.8%; Score 32; DB 12; Length 9;
Best Local Similarity 85.7%; Pred. No. 6.5e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 WGAFTTT 13
Db 2 FGAFTTT 8

RESULT 4
US-09-753-126-100
Sequence 100, Application US/09753126
Patent No. US20020127219A1
GENERAL INFORMATION:
APPLICANT: OKKELS, JENS SIGURD
APPLICANT: JENSEN, ANNE DAM
APPLICANT: HALKIER, TORBEN
APPLICANT: JENSEN, RIKKE BOLDING
```

```
TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
FILE REFERENCE: 31-000600US
CURRENT APPLICATION NUMBER: US/09/753,126
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: PA 1999 01891
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 60/174,652
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: PA 200 00865
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/210,984
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: 60/211,124
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: PA 2000 01027
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/217,497
PRIOR FILING DATE: 2000-07-11
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-753-126-100

Query Match      36.8%; Score 32; DB 10; Length 12;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 APTTND 15
Db 1 APTTND 7

RESULT 5
US-09-896-896A-64
Sequence 64, Application US/09896896A
Publication No. US20030036181A1
GENERAL INFORMATION:
APPLICANT: MAYYGEN APS
TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
FILE REFERENCE: 0217us210
CURRENT APPLICATION NUMBER: US/09/896,896A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/217,497
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: US 60/225,558
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: DK PA 2000 01027
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DK PA 2000 01092
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: PCT/DK00/00743
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: PCT/DK01/00090
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 64
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-896-896A-64

Query Match      36.8%; Score 32; DB 11; Length 12;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 16:30:27 ; Search time 14 Seconds

(without alignments)
48.355 Million cell updates/secTitle: US-09-847-637B-3
Perfect score: 87
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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 133293

Minimum DB seq length: 0
Maximum DB seq length: 16Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	30	34.5	16	4	US-09-500-124-228
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14	27	31.0	15	1	US-07-907-190-8
15	27	31.0	15	1	US-08-320-373-37
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19	26	29.9	8	2	US-08-621-259A-239
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22	26	29.9	8	3	US-09-217-352-237
23	26	29.9	10	2	US-08-556-597-145
24	26	29.9	10	2	US-08-556-597-152
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26	26	29.9	11	1	US-08-293-284A-23
27	26	29.9	11	4	US-08-898-300-23

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30	26	29.9	12	1	US-07-963-321-36	Sequence 36, App1
31	26	29.9	12	1	US-08-290-641-36	Sequence 36, App1
32	26	29.9	12	1	US-08-548-540-36	Sequence 36, App1
33	26	29.9	12	5	PCT-US96-09809-36	Sequence 36, App1
34	26	29.9	14	4	US-08-469-260A-455	Sequence 455, App
35	26	29.9	14	4	US-08-488-446-455	Sequence 455, App
36	26	29.9	14	4	US-08-467-344A-455	Sequence 455, App
37	26	29.9	15	1	US-08-111-939-10	Sequence 21, App1
38	26	29.9	16	1	US-08-307-724B-21	Sequence 21, App1
39	26	29.9	16	3	US-09-242-131A-11	Sequence 11, App1
40	26	29.9	16	4	US-09-615-283-11	Sequence 11, App1
41	25	28.7	6	3	US-08-472-595-6	Sequence 6, App1
42	25	28.7	6	3	US-08-207-575A-6	Sequence 6, App1
43	25	28.7	6	3	US-08-246-441-15	Sequence 15, App1
44	25	28.7	6	4	US-09-393-585-15	Sequence 15, App1
45	25	28.7	7	3	US-08-946-525-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-08-687-590-67
Sequence 67, Application US/08687590
Patent No. 6255070
GENERAL INFORMATION:
APPLICANT: Willison, Keith Robert
APPLICANT: Kubota, Hiroshi
APPLICANT: Ashworth, Alan
TITLE OF INVENTION: Folding Proteins
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,590
FILING DATE: 31-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00192
FILING DATE: 31-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401791.0
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9418234.2
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Baebian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 084619-000000US
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-687-590-67
Query Match 36.8%; Score 32; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TITNDG 16
Db 1 TITNDG 6

RESULT 2

US-09-289-942A-5
; Sequence 5, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pat, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab'-EPTIOPH COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
; FILE REFERENCE: 1038-926 MIS:3b
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-289-942A-5

Query Match 35.6%; Score 31; DB 4; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.5e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 EKKMGAPT 11
Db 2 EDKWDAPS 9

RESULT 3
US-09-336-643A-70
; Sequence 70, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Butler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Primer
US-09-336-643A-70

Query Match 35.6%; Score 31; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 2 KGVVTTTIG 11

RESULT 4

US-08-584-043A-80
; Sequence 80, Application US/08584043A
; Patent No. 6344436
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; APPLICANT: Sparrow, James T.
; APPLICANT: Hauer, Jocheen
; APPLICANT: Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; TITLE OF INVENTION: MACROMOLECULE DELIVERY
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,043A
; FILING DATE: January 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEEX: 67-3510
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-584-043A-80

Query Match 34.5%; Score 30; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LKKKW 7
Db 5 LKKKW 9

RESULT 5

US-08-602-999A-228
; Sequence 228, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.